

SEQUENCE LISTING

<110> Allen, Stephen

<120> Plant Cellulose Synthases

<130> BB1170 US CIP

SAC
1031

<140>

<141>

<150> 60/092,844

<151> 1998-07-14

<150> PCT/US99/15871

<151> 1999-07-13

<150> 09/720383

<151> 2000-12-21

<160> 33

<170> Microsoft Office 97

<210> 1

<211> 1221

<212> DNA

<213> Hordeum vulgare

<400> 1

gcacaggat attcttactg ggtttaaaat gcacgcaaga ggttggatat caatctactg 60
catgccacca cgaccttgtt tcaagggttc tgcgc当地 aatctctctg accgtctcaa 120
tcaagttctc cggtgggctc ttgggtcagt tgaaattctg tttagcagac attgtccat 180
ctggtacaat tacgggtgggc ggttggaaact tctggagagg atggcttaca tcaacaccat 240
tgtttatcca ataacatccc ttccacttat cgcctattt gtgc当地 ctatctgtct 300
cctcaccaac aaatttatca ttcccgagat cagtaactat gctggatgt tctttattct 360
tatgttgcc tccatcttg ccacgggtat attggagctg cgatggagtg gtgc当地 420
cgaggactgg tgagaaaacg agcagttctg gtttattgtt ggcacatctg cccatcttt 480
cgcagtgttc cagggtctgc taaagggtt ggccgggatt gacaccaact tcacggttac 540
ctcgaaggca aacgacgagg atggcattt tgctgagtt tacgtgtca agtggaccag 600
tctcctcatt cctccgacca ccgtcctgt gattaacctg gtggcatgg tggcaggcat 660
atcatatgcc atcaaacagcg gttaccagtc ttggggtcca ctctcggaa agctcttctt 720
ctcaatctgg gtgatcctcc atctctaccc cttcctcaag ggtctcatgg ggaaggcagaa 780
ccgcacccca accatcgtca ttgtttggtc catcctccata gcctccatct tctccctcct 840
gtgggtgaag atcgaccctt tcatatccga taccaggaaa gccgtc当地 tggggcagtg 900
tggcgtcaac tgctgatgg cgccgaagag tatctgcccc cctc当地gttaa ataccggagg 960
gggttggatg ggattttttt gttgttagatg aagacggagt tttatgttaag ttattattgc 1020
cccttc当地gtgc tgagaacac aaaccgtgaa gcctacgaaa cctgc当地gtgt acattgtgat 1080
ttttttctcc ttttcttttc atctgtgata cctgttggg cttcttagag tatattatgt 1140
cagaacgtat ctataacttct atacacacta tgacaccaac tatttatata aggcaactgt 1200
tgc当地tcaact cttctgcaaa a a 1221

<210> 2

<211> 304

<212> PRT

<213> Hordeum vulgare

<400> 2

His Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Ile

1

5

卷之三

TOP SECRET

<400>	3					
gcgcgcgcgc	caggcgcaac	gcaacaagg	gaaacccag	ccggaggagc	aaaagctagc	60
aagcgtgtcc	ctccccctcc	ctcaactccg	tttcattcca	ttccccccc	gacgccgcta	120
ccgcccgcgc	cgcacgcacg	cttgcggccgg	gatctggaga	tctggtagcg	ccagggggat	180
ggaggccagc	gccgggctgg	tcgcccgtc	gcacaaccgg	aacgagctcg	tcgtcatccg	240
ccgcgtatggc	gagccaggcgc	cgaagccat	ggaccagcgg	aacggccagg	tgtccagat	300
ttgcggcgcac	gacgtggggc	gcaacccga	cggggagcgg	ttcgtggct	gcaacgagtg	360
cgccctcccc	atctgcggg	actgtacga	gtacgagcgc	cgcgagggca	cgcagaactg	420
cccccagtgc	aagaccgcct	tcaagcgcct	caaggggtgc	gcgccgtgc	ccggggacga	480
ggaggaggac	ggcgtcgac	acctggagaa	cgagttcaac	tggagcgaca	agcacgactc	540
ccagtatctc	gccgagtcct	tgctccacgc	ccacatgagc	tacgcccgcg	gcccgcacct	600
cgacggcggt	ccgcagccat	tccacccat	ccccatgtt	cccctccca	ccaacggaca	660
gatggtcgtat	gacatcccgc	cggaccagca	cgcccgttg	ccctcggtcg	tgggtggcgg	720
ggggaaagagg	attcaccctc	tcccgtacgc	gatcccaac	cttctgtgc	aaccgaggtc	780
tatggaccct	tccaaggatct	tcgcccata	tggctacggg	agcgtagcat	ggaaggagag	840
gatggagagc	tgaagcaga	agcagagag	gatgcaccag	acgaggaacg	atggcggcgg	900
cgatgtatgt	gatgtatgcag	atctaccact	aatggatgaa	gctagacagc	cattgtccag	960
aaagatcccg	cttccttcata	gccaatcaa	cccctatagg	atgattataa	taattcggtc	1020
agtggtttgc	tgtttcttct	tccactaccg	agtgtatcat	ccgggtgcctg	atgcatttgc	1080
tttatggctc	atatctgtat	tctgtaaat	ttgggttgc	atgtcttgc	ttcttgacca	1140
gtttccaaag	tgtttccata	tcgagaggga	aacctatctt	gaccggctga	gtttaagggtt	1200
tgacaaggaa	gggcattcctt	ctcaactcgc	ccctgttgc	ttcttgatca	gtacgggtga	1260
tcccttgaag	gaacctccat	tggtaactgc	taatactgtt	ctatctatcc	tttcgggtga	1320
ttatccagtt	gataagggtt	catgtacgt	ttctgtatgt	ggtgcgtcga	tgctgacatt	1380
tgaagcattt	tctgaaacat	ctgaatttgc	aaagaaaatgg	gttccttct	gcaaaagata	1440
tagccttgcag	cctcgtgctc	cagagtggta	cttccaaacag	aagatagact	acctgaaaga	1500
caagggtggcg	ccaaactttt	tttagagaacg	gagagcaatg	aagagaggt	atgaggaatt	1560
caagggtcaga	atcaatgcct	tggttctaa	agcccaaaag	gttcctgagg	aaggatggac	1620
aatgcaggat	ggaactccat	ggccggaaa	taatgtccgt	gatcatcctg	aatgtattca	1680
gtttttccctt	ggtcaaagtgt	gtggccatga	tgtggaaagga	aatgagctgc	ctcgatttgt	1740
ttatgtttca	agagaaaaaac	ggccaggcta	caaccatcac	aagaaggctg	gtgctatgaa	1800
tgcattggtc	cgagtctctg	ctgtactaac	taatgtctct	tatttgctga	acttggattg	1860
tgatcactat	atcaataata	gtaaggctat	aaaggaagca	atgtgtttt	tgatggatcc	1920
tttgcttgcg	aagaaagttt	gctatgtgc	gtttcctcaa	agatttgatg	ggatttgatcg	1980
ccatgatcga	tatgctaaca	gaaatgttgt	cttttcgtat	atcaacatga	aaggtttgg	2040
tggatccat	ggcccaattt	atgtgggtac	tggatgtgtc	ttcagaaggc	aggcattata	2100
tggctacgat	gctcccaaaa	caaagaagcc	accatcaaga	acttgcaact	gctggccaaa	2160
gtgggtgcatt	tgctgttgc	gttttgcata	caggaagacc	aagaagaaga	ccaagacctc	2220
taaacctaaa	tttgagaaga	taaagaaact	ttttaagaaaa	aaggaaaatc	aagccctgc	2280
atatgcctt	ggtgaatttgc	atgaagccgc	tccaggagct	gaaaatgaaa	aggctagtat	2340
tgtaaatcaa	cagaagttgg	aaaagaaaatt	tggccagttc	tcagtttttgc	ttgcatccac	2400
acttcttgcag	aatgggtggaa	ccctgaagag	tgccagtcc	gttctcttc	tgaaggaagc	2460
tatacatgtc	atcgtttgt	gatatgaaga	caaaaacaggc	tggggaaaag	atattggtt	2520
gattttatgg	tcagtcacag	aagatattct	tactgggtt	aagatgcact	gccatgggt	2580
gcggtaattt	tactgcatac	ctaaacgggc	cccttccat	gttccgcac	ctctcaatct	2640
ttcccgatcgt	cttcaccagg	ttcttcgttgc	ggcttgcgtt	tcaattgaaa	ttttcttcag	2700
caaccactgc	cctctctgg	atgggtatgg	tgggtggacta	aagttcctgg	aaaggtttc	2760
gtacatataac	tcacatcgat	acccttggac	atctatcccg	ctcttggct	attgcacatt	2820
gcctggccatc	tgcttgcgt	cagggaaattt	tatcacgcac	gagcttaaca	atgttgcag	2880
cctctgttgc	atgtcacttt	tcatctgc	ttttgtacgt	agcatcctgg	aatgagatg	2940
gagttttgtt	ggcatcgat	actgggtgg	aaacgagcag	ttttgggtca	ttggaggcgt	3000
gtcttcacat	ctctttgtct	tgttccagg	actcttcac	gtcatacgct	gtgttagacac	3060
gagttttact	gtgacatcca	agggccggaga	cgacgaggag	ttctcagac	tgtacacatt	3120
caaataatggac	acccttctga	taccccgac	aaccctgtc	ctactgaact	tcattggagt	3180
ggtagcttgc	atctccaatg	cgatcaacaa	cgatcatgaa	tcatggggcc	ccctgttgc	3240
gaagcttctc	tttgcatttt	gggtgatcg	ccatcttac	ccgttccat	agggtcttgc	3300
tggggaggcag	aacaggacgc	caacgattgt	cattgtctgg	tccatccctc	tggcttgc	3360
cttctcgctg	cttgggttc	ggatcgaccc	gttccctgc	aaggatgtat	gtcccctgtt	3420
ggaggagtgt	ggtctggatt	gcaacttagga	ggtcagcag	tggacttccc	cgtcagtg	3480
tggtcgaaga	agtatttttgc	cagatgtttt	gtgcccata	ttctttttc	aatttttg	3540

cctctgtaga tagaaacaag gggagaaggg gaaaaaaaaagt acttgtatcc 3600
atggtgtgg tgggtgggg cggctcagcc tcgtgagtc agtattggc aaaccggagg 3660
ctgcggcaac ctgtgcagt tcggcacga atatactagg gaagatcgcg accaatcaat 3720
caatcgatga ccgagttcaa ttgttcagca aaaaaaaaaaaa aaaaaaaaaa 3776

<210> 4
<211> 1148
<212> PRT
<213> Zea mays

<400> 4
Arg Ala Ala Gln Ala Gln Arg Asn Lys Gly Lys Pro Gln Pro Glu Glu
1 5 10 15

Gln Lys Leu Ala Ser Val Ser Leu Pro Leu Pro His Ser Arg Phe Ile
20 25 30

Pro Phe Pro Pro Arg Arg Tyr Arg Arg Arg Thr His Ala Cys
35 40 45

Pro Gly Ile Trp Arg Ser Gly Ser Ala Arg Gly Met Glu Ala Ser Ala
50 55 60

Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg
65 70 75 80

Arg Asp Gly Glu Pro Gly Pro Lys Pro Met Asp Gln Arg Asn Gly Gln
85 90 95

Val Cys Gln Ile Cys Gly Asp Asp Val Gly Arg Asn Pro Asp Gly Glu
100 105 110

Pro Phe Val Ala Cys Asn Glu Cys Ala Phe Pro Ile Cys Arg Asp Cys
115 120 125

Tyr Glu Tyr Glu Arg Arg Glu Gly Thr Gln Asn Cys Pro Gln Cys Lys
130 135 140

Thr Arg Phe Lys Arg Leu Lys Gly Cys Ala Arg Val Pro Gly Asp Glu
145 150 155 160

Glu Glu Asp Gly Val Asp Asp Leu Glu Asn Glu Phe Asn Trp Ser Asp
165 170 175

Lys His Asp Ser Gln Tyr Leu Ala Glu Ser Met Leu His Ala His Met
180 185 190

Ser Tyr Gly Arg Gly Ala Asp Leu Asp Gly Val Pro Gln Pro Phe His
195 200 205

Pro Ile Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp
210 215 220

Ile Pro Pro Asp Gln His Ala Leu Val Pro Ser Phe Val Gly Gly Gly
225 230 235 240

Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro Asn Leu Pro Val
245 250 255

DRAFT

Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr
260 265 270

Gly Ser Val Ala Trp Lys Glu Arg Met Glu Ser Trp Lys Gln Lys Gln
275 280 285

Glu Arg Met His Gln Thr Arg Asn Asp Gly Gly Asp Asp Gly Asp
290 295 300

Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg
305 310 315 320

Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr Arg Met Ile Ile
325 330 335

Ile Ile Arg Leu Val Val Leu Cys Phe Phe Phe His Tyr Arg Val Met
340 345 350

His Pro Val Pro Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys
355 360 365

Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
370 375 380

Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser Leu Arg Phe
385 390 395 400

Asp Lys Glu Gly His Pro Ser Gln Leu Ala Pro Val Asp Phe Phe Val
405 410 415

Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
420 425 430

Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser Cys
435 440 445

Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu Ser
450 455 460

Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Cys Lys Arg Tyr
465 470 475 480

Ser Leu Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln Lys Ile Asp
485 490 495

Tyr Leu Lys Asp Lys Val Ala Pro Asn Phe Val Arg Glu Arg Arg Ala
500 505 510

Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
515 520 525

Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
530 535 540

Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly Met Ile Gln
545 550 555 560

Val Phe Leu Gly Gln Ser Gly Gly His Asp Val Glu Gly Asn Glu Leu
565 570 575

Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Tyr Asn His
 580 585 590

 His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
 595 600 605

 Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys Asp His Tyr Ile
 610 615 620

 Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met Met Asp Pro
 625 630 635 640

 Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
 645 650 655

 Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn Val Val Phe Phe
 660 665 670

 Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Ile Tyr Val
 675 680 685

 Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr Gly Tyr Asp Ala
 690 695 700

 Pro Lys Thr Lys Lys Pro Pro Ser Arg Thr Cys Asn Cys Trp Pro Lys
 705 710 715 720

 Trp Cys Ile Cys Cys Cys Cys Phe Gly Asn Arg Lys Thr Lys Lys
 725 730 735

 Thr Lys Thr Ser Lys Pro Lys Phe Glu Lys Ile Lys Lys Leu Phe Lys
 740 745 750

 Lys Lys Glu Asn Gln Ala Pro Ala Tyr Ala Leu Gly Glu Ile Asp Glu
 755 760 765

 Ala Ala Pro Gly Ala Glu Asn Glu Lys Ala Ser Ile Val Asn Gln Gln
 770 775 780

 Lys Leu Glu Lys Lys Phe Gly Gln Ser Ser Val Phe Val Ala Ser Thr
 785 790 795 800

 Leu Leu Glu Asn Gly Gly Thr Leu Lys Ser Ala Ser Pro Ala Ser Leu
 805 810 815

 Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys Thr
 820 825 830

 Gly Trp Gly Lys Asp Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp
 835 840 845

 Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg Ser Ile Tyr
 850 855 860

 Cys Ile Pro Lys Arg Ala Ala Phe Lys Gly Ser Ala Pro Leu Asn Leu
 865 870 875 880

 Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly Ser Ile Glu
 885 890 895

Zea mays

Ile	Phe	Phe	Ser	Asn	His	Cys	Pro	Leu	Trp	Tyr	Gly	Tyr	Gly	Gly	Gly
900								905					910		
Leu	Lys	Phe	Leu	Glu	Arg	Phe	Ser	Tyr	Ile	Asn	Ser	Ile	Val	Tyr	Pro
915							920					925			
Trp	Thr	Ser	Ile	Pro	Leu	Leu	Ala	Tyr	Cys	Thr	Leu	Pro	Ala	Ile	Cys
930						935					940				
Leu	Leu	Thr	Gly	Lys	Phe	Ile	Thr	Pro	Glu	Leu	Asn	Asn	Val	Ala	Ser
945					950				955				960		
Leu	Trp	Phe	Met	Ser	Leu	Phe	Ile	Cys	Ile	Phe	Ala	Thr	Ser	Ile	Leu
965							970					975			
Glu	Met	Arg	Trp	Ser	Gly	Val	Gly	Ile	Asp	Asp	Trp	Trp	Arg	Asn	Glu
980							985					990			
Gln	Phe	Trp	Val	Ile	Gly	Gly	Val	Ser	Ser	His	Leu	Phe	Ala	Val	Phe
995							1000					1005			
Gln	Gly	Leu	Leu	Lys	Val	Ile	Ala	Gly	Val	Asp	Thr	Ser	Phe	Thr	Val
1010							1015					1020			
Thr	Ser	Lys	Gly	Gly	Asp	Asp	Glu	Glu	Phe	Ser	Glu	Leu	Tyr	Thr	Phe
1025					1030				1035				1040		
Lys	Trp	Thr	Thr	Leu	Leu	Ile	Pro	Pro	Thr	Thr	Leu	Leu	Leu	Leu	Asn
							1045			1050				1055	
Phe	Ile	Gly	Val	Val	Ala	Gly	Ile	Ser	Asn	Ala	Ile	Asn	Asn	Gly	Tyr
							1060			1065				1070	
Glu	Ser	Trp	Gly	Pro	Leu	Phe	Gly	Lys	Leu	Phe	Phe	Ala	Phe	Trp	Val
							1075			1080				1085	
Ile	Val	His	Leu	Tyr	Pro	Phe	Leu	Lys	Gly	Leu	Val	Gly	Arg	Gln	Asn
							1090			1095				1100	
Arg	Thr	Pro	Thr	Ile	Val	Ile	Val	Trp	Ser	Ile	Leu	Leu	Ala	Ser	Ile
							1105			1110				1115	
Phe	Ser	Leu	Leu	Trp	Val	Arg	Ile	Asp	Pro	Phe	Leu	Ala	Lys	Asp	Asp
							1125			1130				1135	
Gly	Pro	Leu	Leu	Glu	Glu	Cys	Gly	Leu	Asp	Cys	Asn				
							1140			1145					

<210> 5
<211> 1189

<212> DNA

<213> Zea mays

<400> 5
gcacgagacc gagtggggca aggagattgg gtggatctat gggtcggta cagaggat 60
cctgacgggg ttcaagatgc actgccgggg gtggaagtcc gtgtactgca cgccgacacg 120
gccggcggttc aagggggtcgg cgcccataa cttgtctgat cgtctccacc aggtgctgcg 180
ctggggcgctg gggtccgtgg agatcttcat gagccgccac tgcccgctct ggtacgctta 240
cggcggccgg ctcaagtggc tggagcgctt cgcctacacc aacaccatcg tgtacccctt 300
cacctccatc ccgctcctcg cctactgcac catccccgcc gctctgcctgc tcaccggcaa 360

gttcatcatt cccacgctga acaaacctcg cagcatctgg ttcatcgcbc tcttcctgtc 420
 catcatcgcg acgagcgtcc tggagctgcg gtggagcggg gtgagcatcg aggactgtg 480
 ggcgaacgag cagttctgg tcatacgccg cgtgtccgcg catcttgc cctgtttcca 540
 gggcttcctc aagggtctgg gcggcggtga caccagcttc accgtcacct ccaaggcggc 600
 cggcgacgag gccgacgcct tcggggacct ctacctctc aagtggacca ccctgcttgt 660
 gccccccacc acgctcatca tcatcaacat gttgggcatc gtggccggcg tgccgacgc 720
 cgtcaacaac gctacggct cctggggccc gctttcgcc aagctttct tctccttctg 780
 ggtcatcgtc cacctctacc cgatcctcaa ggggctcatg gggaggcaga accggacgcc 840
 caccatcgtc gtgctctgg ccatacctc cgcctccatc ttctcgctcg tctgggtcag 900
 gatcgacccg ttatcccg aggccaaagg cccatccctc aagccatgcg gagtcgagtg 960
 ctgagctcac ctagctacct tcttggca tgtacggacg ccgcgtgcg tttggacata 1020
 caggcacctt tgggcccaggc tactcatgtt cgacttttt ttaattttg tacaagattt 1080
 gtgatcgagt gactgagtga gacagagtgt tgggtgtaa aactgtgtatc gaattcactc 1140
 aaattaatgg acatTTTTT tcttcaactg caaaaaaaaaaaaaaaa 1189

<210> 6
 <211> 320
 <212> PRT
 <213> Zea mays

<400> 6
 His Glu Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Val
 1 5 10 15

 Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys Arg Gly Trp Lys
 20 25 30

 Ser Val Tyr Cys Thr Pro Thr Arg Pro Ala Phe Lys Gly Ser Ala Pro
 35 40 45

 Ile Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly
 50 55 60

 Ser Val Glu Ile Phe Met Ser Arg His Cys Pro Leu Trp Tyr Ala Tyr
 65 70 75 80

 Gly Gly Arg Leu Lys Trp Leu Glu Arg Phe Ala Tyr Thr Asn Thr Ile
 85 90 95

 Val Tyr Pro Phe Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Ile Pro
 100 105 110

 Ala Val Cys Leu Leu Thr Gly Lys Phe Ile Ile Pro Thr Leu Asn Asn
 115 120 125

 Leu Ala Ser Ile Trp Phe Ile Ala Leu Phe Leu Ser Ile Ile Ala Thr
 130 135 140

 Ser Val Leu Glu Leu Arg Trp Ser Gly Val Ser Ile Glu Asp Trp Trp
 145 150 155 160

 Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe
 165 170 175

 Ala Val Phe Gln Gly Phe Leu Lys Val Leu Gly Gly Val Asp Thr Ser
 180 185 190

 Phe Thr Val Thr Ser Lys Ala Ala Gly Asp Glu Ala Asp Ala Phe Gly
 195 200 205

T000000000000000

Asp Leu Tyr Leu Phe Lys Trp Thr Thr Leu Leu Val Pro Pro Thr Thr
 210 215 220

Leu Ile Ile Ile Asn Met Val Gly Ile Val Ala Gly Val Ser Asp Ala
 225 230 235 240

Val Asn Asn Gly Tyr Gly Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe
 245 250 255

Phe Ser Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu
 260 265 270

Met Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Val Leu Trp Ser Ile
 275 280 285

Leu Leu Ala Ser Ile Phe Ser Leu Val Trp Val Arg Ile Asp Pro Phe
 290 295 300

Ile Pro Lys Ala Lys Gly Pro Ile Leu Lys Pro Cys Gly Val Glu Cys
 305 310 315 320

<210> 7

<211> 3786

<212> DNA

<213> Zea mays

<400> 7

ccacagctca	tataccaaga	gccggaggcag	cttagcgca	cccagagcgg	cgcgcgcgcca	60
agcacaaacc	ccacccgcca	cagccgcgtg	cgcatgtgag	cggtcgcgc	ggccgggaga	120
ccagaggagg	ggaggactac	gtcatttcg	ctgtgccgc	gccgcgggt	tcgtgcgcga	180
gcgagatccg	gcggggcggg	gcggggggcc	ttagatggag	gctagcgcgg	ggctgggtgc	240
cggctcgcat	aaccggaacg	agctgttgtt	gatccgcgc	gaccgcgagt	cgggagccgc	300
gggcggcggc	gccccgcgc	ggcggagggc	gccgtgccag	atatgcggcg	acgagggtcg	360
gttgggcttc	gacgggggagc	ccttcgtggc	gtgcaacgag	tgcgccttcc	ccgtctgcgg	420
cgcctgtac	gagtacgagc	gccgcggagg	ctcgcaagcg	tgccgcgcgt	gcaggaccgg	480
ctacaagcgc	ctcaaggggct	gcccgcgggt	ggccggcgac	gaggaggagg	acggcggtcg	540
cgacctggag	ggcgagttcg	gcctgcagga	ccgcgcgcgc	cacgaggacg	acccgcagta	600
cgtcgcgcag	tccatgtcta	gggcgcagat	gagctacggc	cgcgcggcgc	acgcgcaccc	660
cggcttcagc	cccgccccca	acgtgcgcgt	cctcaccac	ggccagatgg	ttgatgacat	720
cccgccggag	cagcacgcgc	tcgtgcgc	ctacatgagc	ggcggcggcg	gcggggggcaa	780
gaggatccac	ccgctccctt	tcgcagatcc	caacccctca	gtcaaccga	gatccatgga	840
cccgtccaag	gatctggccg	cctacggata	ttgcagcgtg	gccttggaaagg	agagaatgga	900
gggcttggaaag	cagaaggcagg	agcgcctgca	gcatgtcagg	agcgagggtg	gcgggtattg	960
ggatggcgac	gatgcagatc	tgccactaat	gatgaaagct	aggcagccat	tgtccagaaa	1020
agtccctata	tcatcaagcc	gaattaatcc	ctacaggatg	attatcgta	tccgggttgt	1080
ggttttgggt	ttcttcttcc	actaccgagt	gatgcaccc	gcgaaagatg	catttgcatt	1140
gtggctcata	tctgtaatct	gtgaaatctg	gttgcgtat	tcctggattc	ttgatcgtt	1200
cccaaagtgg	cttccaatcg	agagagagac	ttacctggac	cgtttgtcac	taaggtttga	1260
caaggaaggt	caaccctctc	agcttgcgtcc	aatcgacttc	tttgcgtat	cgggtgatcc	1320
cacaaaggaa	cctcccttgg	tcacagcgaa	cactgtccct	tccatccctt	ctgtggattt	1380
tccgggttgg	aagggtctcc	gctatgttcc	tgatgatggt	gctgcaatgc	ttacgtttga	1440
agcattgtct	gaaacatctg	aatttgcata	gaaatgggtt	ccttcagca	aaaagttaa	1500
tatcgagcct	cgtgcgtcc	agtggactt	ccaacagaag	atagactacc	tgaaagacaa	1560
ggttgtgtct	tcatttgtta	gggagaggag	ggcgtatgaag	agagaatacg	aggaattcaa	1620
ggttaaggatc	aatgccttgg	ttgcaaaagc	ccaaaagggtt	cctgaggaag	gatggacaat	1680
gcaagatgga	agccctggc	ctggaaacaa	cgtacgcgt	catcctggaa	tgattcagg	1740
attccttggc	caaagtggcg	gtcgtgtatgt	ggaaggaaat	gagttgcctc	gcctgggtta	1800
tgtctcgaga	gaaaagagggc	caggttataa	ccatcacaag	aaggctgtg	ccatgaatgc	1860
actggccgt	gtctctgtcg	tcttatcaa	tgctgcatac	ctattgaact	tggactgtga	1920
tcactacatc	aacaatagca	aggccataaa	agaggctatg	tgtttcatga	tggatccctt	1980

ggtgtgggaag aaagtgtgct atgtacagtt ccctcagagg tttgatggta ttgacaaaaa 2040
tgatcgatac gctaacagga acgttgtctt ttttgacatc aacatgaaag gtttggacgg 2100
tattcaagga cccatttatg tgggtactgg atgtgtttc agacggcagg cactgtatgg 2160
ttatgatgct cctaaaacga agaaggcacc atcaagaact tgcaactgct ggcccaagtg 2220
gtgcctctct tgcgtgtcga gcaggaacaa gaataaaaaag aagactacaa aaccaaagac 2280
ggagaagaag aaaagattat ttttcaagaa acgagaaaaac ccattctcctg catatgctt 2340
gggtgaaatt gatgaagggtg ctccaggtgc tgatatcgag aaggccggaa tcgtaaatca 2400
acagaaaacta gagaagaaat ttgggcagtc ttctgtttt gtcgcataa cacttcttga 2460
gaacggaggg accctgaaga ggcgaagtcc agcttcttctt ctgaaggaag ctatacatgt 2520
tatcagctgc ggctacgaag acaagaccga ctggggaaaa gagattggct ggatttacgg 2580
atcgatcaca gaggatatct tgactggatt taagatgcac tgccatggct ggcggcttat 2640
ttactgcata cccaagcggc ctgcattcaa aggttctgct cctctgaacc ttccgaccg 2700
tcttcaccag gtccctcgct gggcccttgg gtccgtcgaa attttcttca gcaagcactg 2760
cccacttgg tacggatacg gcccgggct aaaattctg gaaaggtttt cttatatcaa 2820
ctccatcggt tatccctgga cgtccattcc tctctggct tactgtacct tgccctccat 2880
ctgcctgctc acggggaaat ttatcacacc agagcttacc aatgtcgcca gtatctggtt 2940
catggcactt ttcatctgca tctccgtgac cggcattctg gaaatgaggt ggagtggcgt 3000
ggccatcgac gactggtggaa ggaacgagca gttctgggtc atcggaggcg ttccggcga 3060
tctgttcgctg gtgttccagg gcctgctgaa ggtgttcgcc ggcatacgaca cgagcttcac 3120
cgtgacgtcg aaggccgggg acgacgagga gttctcgag ctgtacacgt tcaagtggac 3180
caccctgctg atacccccca ccacgctctt cctgctgaac ttcatcgaaa tgggtggcgg 3240
gatctgaac gcatcaaca acgggtacga gtcgtggggc cccctgttcg ggaagcttt 3300
cttcgccttc tgggtgatcg tccacctgta cccgttcctc aagggtctgg tggggaggca 3360
gaacaggacg ccgacgatcg tcatcgctg gtccatctg ctggcctcga tcttctcgct 3420
cctgtgggtc cgcgtcgacc cgttcctcgca caagagcaac ggcccgtcc tggaggagtg 3480
tggcctggac tgaactgaa gtggggccc cctgtcactc gaagttctgt cacggggcga 3540
ttacgcctga tttttgtt ttgttgggtt tggattttt tgctgttagat agaaaccaca 3600
tgtccacggc atctctgctg tgtccattgg agcaggagag aggtgcctgc tgctgtttgt 3660
tgagtaaatt aaaagttta aagtataca gtgatgcaca ttccactgccc cagtgtattc 3720
ccttttaca gtctgtatata tagcgacaaa ggacatattt gtttaggagtt tgattcttt 3780
gtaaaaa 3786

<210> 8

<211> 1165

<212> PRT

<213> Zea mays

<400> 8

His Ser Ser Tyr Thr Lys Ser Arg Ser Ser Leu Ala Gln Pro Arg Ala
1 5 10 15

Ala Pro Arg Gln Ala Gln Pro Pro Pro Ala Thr Ala Ala Cys Ala Cys
20 25 30

Glu Arg Ser Pro Arg Pro Gly Asp Gln Arg Arg Gly Gly Leu Arg Ala
35 40 45

Phe Arg Cys Ala Ala Ala Gly Phe Val Arg Glu Arg Asp Pro Ala
50 55 60

Gly Arg Gly Gly Gly Pro Glu Met Glu Ala Ser Ala Gly Leu Val Ala
65 70 75 80

Gly Ser His Asn Arg Asn Glu Leu Val Val Ile Arg Arg Asp Arg Glu
85 90 95

Ser Gly Ala Ala Gly Gly Ala Ala Arg Arg Ala Glu Ala Pro Cys
100 105 110

Gln Ile Cys Gly Asp Glu Val Gly Val Gly Phe Asp Gly Glu Pro Phe
 115 120 125
 Val Ala Cys Asn Glu Cys Ala Phe Pro Val Cys Arg Ala Cys Tyr Glu
 130 135 140
 Tyr Glu Arg Arg Glu Gly Ser Gln Ala Cys Pro Gln Cys Arg Thr Arg
 145 150 155 160
 Tyr Lys Arg Leu Lys Gly Cys Pro Arg Val Ala Gly Asp Glu Glu Glu
 165 170 175
 Asp Gly Val Asp Asp Leu Glu Gly Glu Phe Gly Leu Gln Asp Gly Ala
 180 185 190
 Ala His Glu Asp Asp Pro Gln Tyr Val Ala Glu Ser Met Leu Arg Ala
 195 200 205
 Gln Met Ser Tyr Gly Arg Gly Gly Asp Ala His Pro Gly Phe Ser Pro
 210 215 220
 Val Pro Asn Val Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp Ile
 225 230 235 240
 Pro Pro Glu Gln His Ala Leu Val Pro Ser Tyr Met Ser Gly Gly
 245 250 255
 Gly Gly Gly Lys Arg Ile His Pro Leu Pro Phe Ala Asp Pro Asn Leu
 260 265 270
 Pro Val Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr
 275 280 285
 Gly Tyr Gly Ser Val Ala Trp Lys Glu Arg Met Glu Gly Trp Lys Gln
 290 295 300
 Lys Gln Glu Arg Leu Gln His Val Arg Ser Glu Gly Gly Asp Trp
 305 310 315 320
 Asp Gly Asp Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro
 325 330 335
 Leu Ser Arg Lys Val Pro Ile Ser Ser Ser Arg Ile Asn Pro Tyr Arg
 340 345 350
 Met Ile Ile Val Ile Arg Leu Val Val Leu Gly Phe Phe Phe His Tyr
 355 360 365
 Arg Val Met His Pro Ala Lys Asp Ala Phe Ala Leu Trp Leu Ile Ser
 370 375 380
 Val Ile Cys Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln Phe
 385 390 395 400
 Pro Lys Trp Leu Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu Ser
 405 410 415
 Leu Arg Phe Asp Lys Glu Gly Gln Pro Ser Gln Leu Ala Pro Ile Asp
 420 425 430

Phe Phe Val Ser Thr Val Asp Pro Thr Lys Glu Pro Pro Leu Val Thr
 435 440 445
 Ala Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Glu Lys
 450 455 460
 Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu
 465 470 475 480
 Ala Leu Ser Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe Ser
 485 490 495
 Lys Lys Phe Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln Gln
 500 505 510
 Lys Ile Asp Tyr Leu Lys Asp Lys Val Ala Ala Ser Phe Val Arg Glu
 515 520 525
 Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn
 530 535 540
 Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met
 545 550 555 560
 Gln Asp Gly Ser Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly
 565 570 575
 Met Ile Gln Val Phe Leu Gly Gln Ser Gly Gly Arg Asp Val Glu Gly
 580 585 590
 Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly
 595 600 605
 Tyr Asn His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val
 610 615 620
 Ser Ala Val Leu Ser Asn Ala Ala Tyr Leu Leu Asn Leu Asp Cys Asp
 625 630 635 640
 His Tyr Ile Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe Met
 645 650 655
 Met Asp Pro Leu Val Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln
 660 665 670
 Arg Phe Asp Gly Ile Asp Lys Asn Asp Arg Tyr Ala Asn Arg Asn Val
 675 680 685
 Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro
 690 695 700
 Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr Gly
 705 710 715 720
 Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser Arg Thr Cys Asn Cys
 725 730 735
 Trp Pro Lys Trp Cys Leu Ser Cys Cys Cys Ser Arg Asn Lys Asn Lys
 740 745 750

Lys Lys Thr Thr Lys Pro Lys Thr Glu Lys Lys Lys Arg Leu Phe Phe
 755 760 765
 Lys Lys Ala Glu Asn Pro Ser Pro Ala Tyr Ala Leu Gly Glu Ile Asp
 770 775 780
 Glu Gly Ala Pro Gly Ala Asp Ile Glu Lys Ala Gly Ile Val Asn Gln
 785 790 795 800
 Gln Lys Leu Glu Lys Lys Phe Gly Gln Ser Ser Val Phe Val Ala Ser
 805 810 815
 Thr Leu Leu Glu Asn Gly Gly Thr Leu Lys Ser Ala Ser Pro Ala Ser
 820 825 830
 Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys
 835 840 845
 Thr Asp Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Ile Thr Glu
 850 855 860
 Asp Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg Ser Ile
 865 870 875 880
 Tyr Cys Ile Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Leu Asn
 885 890 895
 Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly Ser Val
 900 905 910
 Glu Ile Phe Phe Ser Lys His Cys Pro Leu Trp Tyr Gly Tyr Gly Gly
 915 920 925
 Gly Leu Lys Phe Leu Glu Arg Phe Ser Tyr Ile Asn Ser Ile Val Tyr
 930 935 940
 Pro Trp Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Leu Pro Ala Ile
 945 950 955 960
 Cys Leu Leu Thr Gly Lys Phe Ile Thr Pro Glu Leu Thr Asn Val Ala
 965 970 975
 Ser Ile Trp Phe Met Ala Leu Phe Ile Cys Ile Ser Val Thr Gly Ile
 980 985 990
 Leu Glu Met Arg Trp Ser Gly Val Ala Ile Asp Asp Trp Trp Arg Asn
 995 1000 1005
 Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe Ala Val
 1010 1015 1020
 Phe Gln Gly Leu Leu Lys Val Phe Ala Gly Ile Asp Thr Ser Phe Thr
 1025 1030 1035 1040
 Val Thr Ser Lys Ala Gly Asp Asp Glu Glu Phe Ser Glu Leu Tyr Thr
 1045 1050 1055
 Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Leu
 1060 1065 1070

Zea mays

Asn Phe Ile Gly Val Val Ala Gly Ile Ser Asn Ala Ile Asn Asn Gly
 1075 1080 1085

Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp
 1090 1095 1100

Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly Arg Gln
 1105 1110 1115 1120

Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu Ala Ser
 1125 1130 1135

Ile Phe Ser Leu Leu Trp Val Arg Val Asp Pro Phe Leu Ala Lys Ser
 1140 1145 1150

Asn Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys Asn
 1155 1160 1165

<210> 9
 <211> 3936
 <212> DNA
 <213> Zea mays

<400> 9
 cttctccctc gtcgggtcgaa cgtggcgccg ctcggcggtc ggtggaaaac cactcgaaaa 60
 atgaggatct gtcgttagag tgagaggagc tacggtaagt atccctctgcc ttcgtcgccg 120
 gcggaaagtgg agggggaggaa gcgttggagg cgagcgccgg gctgggtggcc ggctccccaca 180
 accgcaacga gtcgtcggtc atccgcgcg acggcgatcc cggggcgaag ccggccgggg 240
 agcagaacgg gcagggtgtc cagattgtcg ggcacgacgt cggccgttgc cccggcgaaaa 300
 acccccttcgt ggcgtgcaac gagtgccgttcccccgtctg cggggactgc tacgaatacg 360
 agcggccggaa gggcacgcag aactgcccccc agtgcaagac tcgatatacg cgcctcaagg 420
 gctgccaacg tggaccgtt gacgaggagg aggacggcgt cgatgacactg gacaacgagt 480
 tcaactggaa cggccatgac tcgcgttgc tggccgagtc catgctctac gcccacatga 540
 gctacggccg tggaggtgac cctaattggcg cggccacaagc ttccagctc aaccccaatg 600
 ttccactcct caccacggg caaatggttt atgacatccc accggaggcag cacgcgttgc 660
 tgccttcctt catgggttgtt gggggaaaga ggatacatcc ctttccttat gggatccca 720
 gtttacgttgc gcaacccagg tctatggacc catccaaggaa tcttgcgtca tatgggtatg 780
 gtagtgttgc ttggaaggaa cggatggaga attgaaagca gagacaagag aggtatgcacc 840
 agacggggaa tggatggatg ggtgtatgc tgacgtatgc tgatctacca ctaatggatg 900
 aagcaagaca acaactgtcc agggaaaattt cacttccatc aagccagatt aatccatata 960
 ggatgattat cattattcggtt ctgtgggtt tgggttctt ctccactac cgagtgtatgc 1020
 atccgggttgc gatgttgcatt gctttgtggc tcatatctgt tatctgttgc atctggttt 1080
 ccatgttgc gattttgtat caattccaa atgggttccc tattggaga gagacttacc 1140
 tagaccggct gtcactgagg ttgcacaagg aaggccagcc atctcaactt gctccaattt 1200
 atttcttgcgtt cagttacgggtt gatcccttaa aggaacctcc tttggtcaca acaaataactg 1260
 ttctatctat ctttcgggtt gattatcctg ttgataaggat ttcttgcstat gtttctgtat 1320
 atgggtctgc aatgttcaacg ttgttgcatt tatctgttgc tatctgttgc atctggatg 1380
 gggttccctt ctgcaaaacgg tacaatattt aacccgtcgcc tccagagtgg tacttccaaac 1440
 agaagataga ctacttgaaa gacaagggtgg cagcaaaactt tgtagggag aggagagcaa 1500
 tgaagagaga gtatgaggaa ttcaagggtga gaatcaatgc cttatgttgc aaagcccgaga 1560
 aagttctgttca aagaaggatgg acaatgtcaag atggaaacccc ctggcttggaa aacaatgtt 1620
 gtgtatccatcc tggatgttgc cagggtttcc ttggccaaag cggaggccctt gactgttgg 1680
 gaaatgttgcgtt gtttgcgtt cttagagagaa acggccaggc tataaccatc 1740
 ataagaaaggc tgggttgcgtt aatgttgcgtt tccggatgttgc tgctgtacta acaaataactg 1800
 catattttgtt aaacttggat tggatgttgc tttttttttt tttttttttt tttttttttt 1860
 caatgttgcgtt tatgttgcgtt cttttttttt tttttttttt tttttttttt tttttttttt 1920
 aaagatttgcgtt tgggttgcgtt cggccatgttcaaa gatatgttcaaa cggaaatgtt gtctttttttt 1980
 atatcaacat gaaagggtttt gatgttgcgtt aagggttcaat ttatgttgcgtt actggatgtt 2040
 tattttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt 2100
 ggacttgcaat cttgttgcgtt aatgttgcgtt tttttttttt tttttttttt tttttttttt tttttttttt 2160

aaaagaagac taccaaacc aaaacagaga agaaaaagg attattttc aagaaagaag 2220
agaaccaatc ccctgcatat gctctggc aattgacga agctgctcca ggagctgaga 2280
atgaaaaggc cgttattgt aatcaacaaa aattagaaaa gaaatttgc caatcttcg 2340
ttttgttac atccacactt ctcgagaatg gtggAACCTT gaagagtgc agtccctgctt 2400
ctctttgaa agaagctata catgtcatta gttgtggta tgaagacaag acagactgg 2460
aaaaagagat tgctggatc tatggatcag ttacagaaga tattctaact ggttcaaga 2520
tgcattgtca tggttggcg tcaatttact gcatacctaa acgggttgc ttcaaagg 2580
ctgcacctct gaatcttc gatcgcttc accaggtgc tcgggtggct cttgggtcta 2640
ttgagatctt cttagcaat cattggccctc tttgttatgg gtatggg ggctgaaat 2700
tttggaaag atttcctac atcaactcca tcgtgtatcc ttggacatct attccctct 2760
tggcttactg tacattgcct gccatctgtt tattgacagg gaaatttac actccagagc 2820
tgaataatgt tgccagcctg tggttcatgt cacttttat ctgcatttt gctacgagc 2880
tcctagaaat gagatggagt ggtgtggaa ttgatgactg gtggaggaat gagcagttct 2940
gggtcattgg agtgtgtgtc tcacacctct ttgctgtgtt ccagggactt ctcaagg 3000
tagctgtgt tgatacaagc ttcaccgtga catcaaagg tggagatgat gaggagttct 3060
cagagctata tacattcaaa tggactacct tattgatacc tcctaccacc ttgcttctat 3120
tgaacttcat tgggtggc gctggcg caaatgcgt caataacgg tatgagtc 3180
ggggccccct cttggaaag ctatttttgc cattttgggt gattgtccat ctttatccct 3240
ttctcaaaagg ttgggtggaa aggcaaaaca ggacaccaac gattgtc gtctgg 3300
ttctgctggc ttcaatcttc tcgctcc gggttcggat tgatcttc cttgc 3360
atgatggtcc gttcttgag gagtgtgg tggattgca ctaggatgtc agtgc 3420
ctcccccaat ctgcataatgc ttgaagtata tttctgg tttgc 3480
ctgttagataa gagacatgaa atgtccaaag tttctttga tccatgg acctactt 3540
tatctgagag atatactggg ggaaaatgg ggctgcggc atccttgc agttggccg 3600
tggatatacg catatgc tgtttattt tgc tttattactt gtgc 3660
tagatggct gagccgaaca gcaagg ttgattctgc actgc 3720
tggctctcaa taaggcaggc aggaatgc ctgccc aacagagca cctgc 3780
atttatgtat gcctgttcat tggagg gttca tgg tactagaaat 3840
aacagaatat tagcattaa ctata ttaaagtatg taatgc tg 3900
tgtgtactgt aatcatctga gttgg tgaaaa 3936

<210> 10

<211> 1086

<212> PRT

<213> Zea mays

<400> 10

Met	Glu	Ala	Ser	Ala	Gly	Leu	Val	Ala	Gly	Ser	His	Asn	Arg	Asn	Glu
1								10						15	

Leu	Val	Val	Ile	Arg	Arg	Asp	Gly	Asp	Pro	Gly	Pro	Lys	Pro	Pro	Arg
								20				25		30	

Glu	Gln	Asn	Gly	Gln	Val	Cys	Gln	Ile	Cys	Gly	Asp	Asp	Val	Gly	Leu
								35				40		45	

Ala	Pro	Gly	Gly	Asp	Pro	Phe	Val	Ala	Cys	Asn	Glu	Cys	Ala	Phe	Pro
								50				55		60	

Val	Cys	Arg	Asp	Cys	Tyr	Glu	Tyr	Glu	Arg	Arg	Glu	Gly	Thr	Gln	Asn
								65				70		75	80

Cys	Pro	Gln	Cys	Lys	Thr	Arg	Tyr	Lys	Arg	Leu	Lys	Gly	Cys	Gln	Arg
								85				90		95	

Val	Thr	Gly	Asp	Glu	Glu	Asp	Gly	Val	Asp	Asp	Leu	Asp	Asn	Glu	
								100				105		110	

Phe	Asn	Trp	Asp	Gly	His	Asp	Ser	Gln	Ser	Val	Ala	Glu	Ser	Met	Leu
								115				120		125	

D99000E7-Z00Z00

Tyr Gly His Met Ser Tyr Gly Arg Gly Gly Asp Pro Asn Gly Ala Pro
130 135 140
Gln Ala Phe Gln Leu Asn Pro Asn Val Pro Leu Leu Thr Asn Gly Gln
145 150 155 160
Met Val Asp Asp Ile Pro Pro Glu Gln His Ala Leu Val Pro Ser Phe
165 170 175
Met Gly Gly Gly Lys Arg Ile His Pro Leu Pro Tyr Ala Asp Pro
180 185 190
Ser Leu Pro Val Gln Pro Arg Ser Met Asp Pro Ser Lys Asp Leu Ala
195 200 205
Ala Tyr Gly Tyr Gly Ser Val Ala Trp Lys Glu Arg Met Glu Asn Trp
210 215 220
Lys Gln Arg Gln Glu Arg Met His Gln Thr Gly Asn Asp Gly Gly
225 230 235 240
Asp Asp Gly Asp Asp Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln
245 250 255
Gln Leu Ser Arg Lys Ile Pro Leu Pro Ser Ser Gln Ile Asn Pro Tyr
260 265 270
Arg Met Ile Ile Ile Ile Arg Leu Val Val Leu Gly Phe Phe Phe His
275 280 285
Tyr Arg Val Met His Pro Val Asn Asp Ala Phe Ala Leu Trp Leu Ile
290 295 300
Ser Val Ile Cys Glu Ile Trp Phe Ala Met Ser Trp Ile Leu Asp Gln
305 310 315 320
Phe Pro Lys Trp Phe Pro Ile Glu Arg Glu Thr Tyr Leu Asp Arg Leu
325 330 335
Ser Leu Arg Phe Asp Lys Glu Gly Gln Pro Ser Gln Leu Ala Pro Ile
340 345 350
Asp Phe Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val
355 360 365
Thr Thr Asn Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp
370 375 380
Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe
385 390 395 400
Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala Lys Lys Trp Val Pro Phe
405 410 415
Cys Lys Arg Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gln
420 425 430
Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Ala Ala Asn Phe Val Arg
435 440 445

Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile
 450 455 460
 Asn Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr
 465 470 475 480
 Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro
 485 490 495
 Gly Met Ile Gln Val Phe Leu Gly Gln Ser Gly Gly Leu Asp Cys Glu
 500 505 510
 Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro
 515 520 525
 Gly Tyr Asn His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg
 530 535 540
 Val Ser Ala Val Leu Thr Asn Ala Pro Tyr Leu Leu Asn Leu Asp Cys
 545 550 555 560
 Asp His Tyr Ile Asn Asn Ser Lys Ala Ile Lys Glu Ala Met Cys Phe
 565 570 575
 Met Met Asp Pro Leu Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro
 580 585 590
 Gln Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr Ala Asn Arg Asn
 595 600 605
 Val Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly
 610 615 620
 Pro Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr
 625 630 635 640
 Gly Tyr Asp Ala Pro Lys Thr Lys Lys Pro Pro Ser Arg Thr Cys Asn
 645 650 655
 Cys Trp Pro Lys Trp Cys Phe Cys Cys Cys Cys Phe Gly Asn Arg Lys
 660 665 670
 Gln Lys Lys Thr Thr Lys Pro Lys Thr Glu Lys Lys Lys Leu Leu Phe
 675 680 685
 Phe Lys Lys Glu Glu Asn Gln Ser Pro Ala Tyr Ala Leu Gly Glu Ile
 690 695 700
 Asp Glu Ala Ala Pro Gly Ala Glu Asn Glu Lys Ala Gly Ile Val Asn
 705 710 715 720
 Gln Gln Lys Leu Glu Lys Lys Phe Gly Gln Ser Ser Val Phe Val Thr
 725 730 735
 Ser Thr Leu Leu Glu Asn Gly Gly Thr Leu Lys Ser Ala Ser Pro Ala
 740 745 750
 Ser Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp
 755 760 765

Lys Thr Asp Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr
 770 775 780
 Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys His Gly Trp Arg Ser
 785 790 795 800
 Ile Tyr Cys Ile Pro Lys Arg Val Ala Phe Lys Gly Ser Ala Pro Leu
 805 810 815
 Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly Ser
 820 825 830
 Ile Glu Ile Phe Phe Ser Asn His Cys Pro Leu Trp Tyr Gly Tyr Gly
 835 840 845
 Gly Gly Leu Lys Phe Leu Glu Arg Phe Ser Tyr Ile Asn Ser Ile Val
 850 855 860
 Tyr Pro Trp Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Leu Pro Ala
 865 870 875 880
 Ile Cys Leu Leu Thr Gly Lys Phe Ile Thr Pro Glu Leu Asn Asn Val
 885 890 895
 Ala Ser Leu Trp Phe Met Ser Leu Phe Ile Cys Ile Phe Ala Thr Ser
 900 905 910
 Ile Leu Glu Met Arg Trp Ser Gly Val Gly Ile Asp Asp Trp Trp Arg
 915 920 925
 Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ser His Leu Phe Ala
 930 935 940
 Val Phe Gln Gly Leu Leu Lys Val Ile Ala Gly Val Asp Thr Ser Phe
 945 950 955 960
 Thr Val Thr Ser Lys Gly Gly Asp Asp Glu Glu Phe Ser Glu Leu Tyr
 965 970 975
 Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Leu
 980 985 990
 Leu Asn Phe Ile Gly Val Val Ala Gly Val Ser Asn Ala Ile Asn Asn
 995 1000 1005
 Gly Tyr Glu Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe
 1010 1015 1020
 Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Val Gly Arg
 1025 1030 1035 1040
 Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp Ser Ile Leu Leu Ala
 1045 1050 1055
 Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Leu Ala Lys
 1060 1065 1070
 Asp Asp Gly Pro Leu Leu Glu Glu Cys Gly Leu Asp Cys Asn
 1075 1080 1085

```

<210> 11
<211> 1138
<212> DNA
<213> Oryza sativa

<400> 11
cgctgctccc ggcgatggac gtgttcgtca ccaccgccga cccccacaag gagccgcccgc 60
tcgcccacggc gaacaccgtg ctgtccatat atcctcgccg cgggctaccc cgccggcaag 120
gtgacgtgct atatttccga cgacgcaggc gcggagggtga cacgtaacgc ggtcgtggag 180
gcggcccggt tcgcggcgct ttgggtgtcg ttctgcccga agcacggcgt cgagccgagg 240
aacctggagg cgtacttcaa cgccggcgag ggtggtggtg gcaaggcga ggtgggtggcg 300
agggggagct acagggggat ggcgtggccg gagctggtgc ggcacaggag acgggtgcgc 360
cgcgagtagc aggagatgcg gctgcggatc gacgcgtgc aggccgcccga tgcgcgcgc 420
cggcgcgcgc ggcggccga tgaccacgcc ggagttgtgc aggtactgat cgattttgtct 480
gggagcgtgc cacagctcg cggtgcgaac gggagcaagc tcatcgacgt cgccctgtc 540
gacgtgtgcc tcccgccgt tggtaacgtg tgccgcgaga agcgcgcgg ccacgcgcac 600
caccggaaagg cgggcgcgc cat gaacgcgcgc ttcatcctcg acctcgactg cgactactac 660
gtcaacaact cgaggccct ccgcgcgcgc atctgtttca tgatcgaaacg cggcggcgcc 720
ggagccgcgc aagacgcgcg cgccgtcg cggtccagt tccgcagcg ggtcgacggc 780
gtcgatcccc ggcacgccta cgccaaccac aaccgcgtcc tcttcgactg caccgagetc 840
ggcctcgacg gcctccaggc ccccatctac gtcggcaccg gctgctgtt ccgcgcgtc 900
gcgccttaca gcgtcgacct gccgcgtgg agaccgcggc gttcattggg ctgtcgctta 960
ctcgagaaag acgagcggct atggtccagg atgaaacaaa tggtaatatt aagtggtcca 1020
aggtgaaaaaa cttagctaaa acctgaccca agctgtaaaca tggtaaaaaa tatatggccc 1080
aaaatgaaat ttactttttt ttttttacca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1138

<210> 12
<211> 341
<212> PRT
<213> Oryza sativa

<400> 12
Arg Cys Ser Arg Arg Trp Thr Cys Ser Ser Pro Pro Pro Pro Thr Pro Thr
 1           5           10          15

Arg Ser Arg Arg Ser Pro Arg Arg Thr Pro Cys Cys Pro Tyr Ile Leu
 20          25          30

Ala Ala Gly Tyr Pro Ala Gly Lys Val Thr Cys Tyr Ile Ser Asp Asp
 35          40          45

Ala Gly Ala Glu Val Thr Arg Asn Ala Val Val Glu Ala Ala Arg Phe
 50          55          60

Ala Ala Leu Trp Val Ser Phe Cys Arg Lys His Gly Val Glu Pro Arg
 65          70          75          80

Asn Leu Glu Ala Tyr Phe Asn Ala Gly Glu Gly Gly Gly Lys Ala
 85          90          95

Lys Val Val Ala Arg Gly Ser Tyr Arg Gly Met Ala Trp Pro Glu Leu
100         105         110

Val Arg Asp Arg Arg Val Arg Arg Glu Tyr Glu Glu Met Arg Leu
115         120         125

Arg Ile Asp Ala Leu Gln Ala Ala Asp Ala Arg Arg Arg Arg Arg Gly
130         135         140

```

Ala Ala Asp Asp His Ala Gly Val Val Gln Val Leu Ile Asp Phe Ala
 145 150 155 160
 Gly Ser Val Pro Gln Leu Gly Val Ala Asn Gly Ser Lys Leu Ile Asp
 165 170 175
 Val Ala Ser Val Asp Val Cys Leu Pro Ala Leu Val Tyr Val Cys Arg
 180 185 190
 Glu Lys Arg Arg Gly His Ala His Arg Lys Ala Gly Ala Met Asn
 195 200 205
 Ala Pro Phe Ile Leu Asp Leu Asp Cys Asp Tyr Tyr Val Asn Asn Ser
 210 215 220
 Gln Ala Leu Arg Ala Gly Ile Cys Phe Met Ile Glu Arg Gly Gly
 225 230 235 240
 Gly Ala Ala Glu Asp Ala Gly Ala Val Ala Phe Val Gln Phe Pro Gln
 245 250 255
 Arg Val Asp Gly Val Asp Pro Gly Asp Arg Tyr Ala Asn His Asn Arg
 260 265 270
 Val Leu Phe Asp Cys Thr Glu Leu Gly Leu Asp Gly Leu Gln Gly Pro
 275 280 285
 Ile Tyr Val Gly Thr Gly Cys Leu Phe Arg Arg Val Ala Leu Tyr Ser
 290 295 300
 Val Asp Leu Pro Arg Trp Arg Pro Arg Arg Ser Leu Gly Cys Arg Leu
 305 310 315 320
 Leu Gly Glu Asp Glu Arg Leu Trp Ser Arg Met Lys Gln Met Val Ile
 325 330 335
 Leu Ser Gly Pro Arg
 340
 <210> 13
 <211> 3517
 <212> DNA
 <213> Glycine max
 <400> 13
 gcacgagcca acaacaacac ccttatgtgg acacattagg tgaggttcaa cagctagcac 60
 caatcttcct tcataaaaaca caaacctttg atcacacaat ctcacacctaa tttgtgttgt 120
 tttgtgtcca ttccccatatt gtcccatatt ctaagacatg gaagccagcg ctggacttgt 180
 cgctgggtca cataaccgcata atgagctagt tgcattcat ggccatgaag agccgaaggc 240
 tttgaagaac ttggatgggc aagtgtgtga gatttggtgt gatggcgtgg gactcacggt 300
 ggatggagac ttgttgtgg cttgcaatga gtgtggttt ccagtgtgca ggccttgcta 360
 tgagtatgaa aggagagaag gaagccacct ttgcccacag tgcaaaacca gatacaagcg 420
 tctcaaaggg agcccccgag tggaggggaga tggatgtgaa gaggatgtgg atgatattga 480
 gcatgaattc aatattgtat agcaaaaagaa caagcatggc caggttgcag aagccatgct 540
 tcatgggagg atgagctatg gaagagggtcc tgaagatgtat gacaattccc agttcccaac 600
 acctgtcatt gctgggtggc gttctaggcc tgtaagtggg gagttcccaa tatcatctaa 660
 tgcttatggg gatcagatgt tattcccttc actgcataaaa agatgtgcattc catatccagt 720
 gtctgaacct ggaagtgcac gatgggacga aaaaaaaaaaaa agatggatgg aaagatagaa 780
 tggatgactg gaaattgcag caaggcaatt tggggcctga accggatgaa gatccagatg 840
 cagccatgtt agatgaagca aggcaaccac tgtcaaggaa agtgcataa gcatccagca 900

Digitized by srujanika@gmail.com

aatcaatcc	atatacgttgc	gtgattgtgg	cacgtctgg	tatttttgttgc	ttcttcctca	960
gatacagact	catgaaccca	gtacatgtat	ccctggggct	atggctaacc	tctatcatat	1020
gtgaaatctg	gttgctttt	tcatggattc	tggatcagt	tcccaaattgg	tttcccattg	1080
ata gagagac	ctaccttgc	cgtcttcca	ttaggtatga	gcgtgaagg	gaaccacaaaca	1140
tgcttgc	tgttagatgtt	tttggtagta	ccgtggatcc	catgaaggaa	cctctctgg	1200
ttacagcaaa	cactgttctt	tcaatcttgg	ccatggatta	cccggttcat	aaaatatcat	1260
gctacattc	tgatgtgga	gcctcaatgt	gtacatttg	gtccttatca	gaaactgcag	1320
agtttgc	aaagtggta	ccgtttgt	agaaattttc	catagaaccc	cgggcaccc	1380
agatgtactt	cagcgagaag	attgactacc	taaaggacaa	agtgcacccc	acctttgtt	1440
aggagcgtcg	agctatgaag	aggaaatacg	aagagttaa	ggttaggatc	aatgcactt	1500
ttgctaaggc	ccagaaagtt	cctcagggag	gatggatcat	gcaggatggg	acaccatggc	1560
cagggataaa	cactaaggat	catccttgc	tgattcaagt	gtttcttgg	agcagtggag	1620
gtcttgcatac	tgaaggaaac	caacttcctc	gccttgc	tgtttccaga	gagaaaaggc	1680
ctgggtttca	acaccacaag	aaagctgg	ccatgaatgc	tctgggtcgg	gtatctgc	1740
ttctcaca	ttctccttgc	atgttgcact	tggattgt	tcactatgtc	aataacagca	1800
aggctgccc	agaggccat	tgcttgc	tggaccac	aactggaa	aaggctgt	1860
atgtccagtt	tcctcaaa	tttgatgt	ttgatcaca	tgatcgttat	gcacacagg	1920
acacagttt	cttgatatt	aacatgaagg	gtctagatgg	tattcaagg	cctgtatat	1980
tggggactgg	atgttttc	aggaggcaag	cttgc	ctataatcct	cccaagggtc	2040
caaagcgtcc	aaaaatggta	agctgtgatt	gttgc	tttggaa	cgcaaga	2100
ataaggagaa	gaatgtgca	aatggagagg	ctgcaagcc	aaaaggatg	gatgtgaca	2160
aagagggtt	gatgtccaa	atgaatttt	agaagaaatt	tggacaatcc	tctat	2220
tgacttctac	cttgatggaa	gagggtgg	tgcctc	ttcaagtcc	gtgc	2280
ttaaagaagc	cattcatgt	attagctgt	gatatgaa	taaaactgaa	tgggactt	2340
agcttgc	gatctatgc	tctatcacag	aagatattc	aacagg	aatgtgcatt	2400
gccgtgggt	gaggtccatt	tattgtatgc	caaagagac	tgcattca	gttactgc	2460
ctatcaactt	gtcagatcgt	ctcaaccagg	ttttcg	ggcacttgg	tccattgaga	2520
ttttcttgc	tcaccattgc	cctctatgt	atggcttca	ggaaaaga	ctaaagtgc	2580
ttgagagatt	tccttatgc	aacacaactg	tctatccatt	caccc	cctctatgt	2640
cctactgtat	tcttccagca	gttgc	tcactgacaa	attcatcat	ccaccgatta	2700
gcaccttgc	tggttgc	tttgc	tcttctc	aatcattgca	actgttattc	2760
ttgagttgaa	atggagtgg	gtgagcatt	aggaatgg	gagaaatgag	cagtttgg	2820
tcattgg	tgtatcagct	caccc	ctgttataca	aggtctg	aaggcttctt	2880
ctggaaattga	caccaattt	actgttacat	caaaggca	agatgtgaa	gagtttgg	2940
aattgtacac	ctttaagtgg	actacactct	tgattc	aaccactatt	ttgatcatta	3000
acattgttgg	tgttgc	ggaatctc	atgcataaa	caatgg	caatcctgg	3060
gaccactt	tgaaagctc	ttcttgc	tctgggt	tgtccatctc	tatccatttcc	3120
ttaaagg	gatgggtc	caaattgc	caccc	tgttg	tggtc	3180
tattggctc	tatttctcc	ttacttgg	taagaattg	tccatttgc	ctcaagacta	3240
agggac	taccaagct	tgtggatc	actgtcaaaa	aagactgtt	tccctataat	3300
attattctt	aaaagatgt	tgttaggtac	atacattct	ggttcc	accaacaa	3360
tggcaatgc	caaggatcaa	taaggaaaga	gtaaaattt	tgtgtatcat	aatgaggt	3420
tatcatttt	gtaaaatgtt	tcaaggacat	ctgtttgg	tggaactg	caaaaattgc	3480
aqtttatct	attcactq	aaaaaaaa	aaaaaaa	aaaaaaa		3517

<210> 14
<211> 1039
<212> PRT
<213> Glycine max

<220>
<221> UNSURE
<222> (201)

<400> 14
Met Glu Ala Ser Ala Gly Leu Val Ala Gly Ser His Asn Arg Asn Glu
1 5 10 15

Asp Gly Gln Val Cys Glu Ile Cys Gly Asp Gly Val Gly Leu Thr Val
 35 40 45
 Asp Gly Asp Leu Phe Val Ala Cys Asn Glu Cys Gly Phe Pro Val Cys
 50 55 60
 Arg Pro Cys Tyr Glu Tyr Glu Arg Arg Glu Gly Ser His Leu Cys Pro
 65 70 75 80
 Gln Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Ser Pro Arg Val Glu
 85 90 95
 Gly Asp Asp Asp Glu Glu Asp Val Asp Asp Ile Glu His Glu Phe Asn
 100 105 110
 Ile Asp Glu Gln Lys Asn Lys His Gly Gln Val Ala Glu Ala Met Leu
 115 120 125
 His Gly Arg Met Ser Tyr Gly Arg Gly Pro Glu Asp Asp Asp Asn Ser
 130 135 140
 Gln Phe Pro Thr Pro Val Ile Ala Gly Gly Arg Ser Arg Pro Val Ser
 145 150 155 160
 Gly Glu Phe Pro Ile Ser Ser Asn Ala Tyr Gly Asp Gln Met Leu Ser
 165 170 175
 Ser Ser Leu His Lys Arg Val His Pro Tyr Pro Val Ser Glu Pro Gly
 180 185 190
 Ser Ala Arg Trp Asp Glu Lys Lys Xaa Asp Gly Trp Lys Asp Arg Met
 195 200 205
 Asp Asp Trp Lys Leu Gln Gln Gly Asn Leu Gly Pro Glu Pro Asp Glu
 210 215 220
 Asp Pro Asp Ala Ala Met Leu Asp Glu Ala Arg Gln Pro Leu Ser Arg
 225 230 235 240
 Lys Val Pro Ile Ala Ser Ser Lys Ile Asn Pro Tyr Arg Met Val Ile
 245 250 255
 Val Ala Arg Leu Val Ile Leu Ala Phe Phe Leu Arg Tyr Arg Leu Met
 260 265 270
 Asn Pro Val His Asp Ala Leu Gly Leu Trp Leu Thr Ser Ile Ile Cys
 275 280 285
 Glu Ile Trp Phe Ala Phe Ser Trp Ile Leu Asp Gln Phe Pro Lys Trp
 290 295 300
 Phe Pro Ile Asp Arg Glu Thr Tyr Leu Asp Arg Leu Ser Ile Arg Tyr
 305 310 315 320
 Glu Arg Glu Gly Glu Pro Asn Met Leu Ala Pro Val Asp Val Phe Val
 325 330 335
 Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu Val Thr Ala Asn Thr
 340 345 350

□□□□□□□□□□

Val Leu Ser Ile Leu Ala Met Asp Tyr Pro Val Asp Lys Ile Ser Cys
355 360 365

Tyr Ile Ser Asp Asp Gly Ala Ser Met Cys Thr Phe Glu Ser Leu Ser
370 375 380

Glu Thr Ala Glu Phe Ala Arg Lys Trp Val Pro Phe Cys Lys Lys Phe
385 390 395 400

Ser Ile Glu Pro Arg Ala Pro Glu Met Tyr Phe Ser Glu Lys Ile Asp
405 410 415

Tyr Leu Lys Asp Lys Val Gln Pro Thr Phe Val Lys Glu Arg Arg Ala
420 425 430

Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn Ala Leu Val
435 440 445

Ala Lys Ala Gln Lys Val Pro Gln Gly Gly Trp Ile Met Gln Asp Gly
450 455 460

Thr Pro Trp Pro Gly Asn Asn Thr Lys Asp His Pro Gly Met Ile Gln
465 470 475 480

Val Phe Leu Gly Ser Ser Gly Gly Leu Asp Thr Glu Gly Asn Gln Leu
485 490 495

Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln His
500 505 510

His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala Val
515 520 525

Leu Thr Asn Ala Pro Phe Met Leu Asn Leu Asp Cys Asp His Tyr Val
530 535 540

Asn Asn Ser Lys Ala Ala Arg Glu Ala Met Cys Phe Leu Met Asp Pro
545 550 555 560

Gln Thr Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
565 570 575

Gly Ile Asp Thr His Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe Phe
580 585 590

Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr Val
595 600 605

Gly Thr Gly Cys Val Phe Arg Arg Gln Ala Leu Tyr Gly Tyr Asn Pro
610 615 620

Pro Lys Gly Pro Lys Arg Pro Lys Met Val Ser Cys Asp Cys Cys Pro
625 630 635 640

Cys Phe Gly Ser Arg Lys Lys Tyr Lys Glu Lys Asn Asp Ala Asn Gly
645 650 655

Glu Ala Ala Ser Leu Lys Gly Met Asp Asp Asp Lys Glu Val Leu Met
660 665 670

Ser Gln Met Asn Phe Glu Lys Lys Phe Gly Gln Ser Ser Ile Phe Val
 675 680 685
 Thr Ser Thr Leu Met Glu Glu Gly Gly Val Pro Pro Ser Ser Ser Pro
 690 695 700
 Ala Ala Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu
 705 710 715 720
 Asp Lys Thr Glu Trp Gly Leu Glu Leu Gly Trp Ile Tyr Gly Ser Ile
 725 730 735
 Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys Arg Gly Trp Arg
 740 745 750
 Ser Ile Tyr Cys Met Pro Lys Arg Ala Ala Phe Lys Gly Thr Ala Pro
 755 760 765
 Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly
 770 775 780
 Ser Ile Glu Ile Phe Phe Ser His His Cys Pro Leu Trp Tyr Gly Phe
 785 790 795 800
 Lys Glu Lys Lys Leu Lys Trp Leu Glu Arg Phe Ala Tyr Ala Asn Thr
 805 810 815
 Thr Val Tyr Pro Phe Thr Ser Ile Pro Leu Val Ala Tyr Cys Ile Leu
 820 825 830
 Pro Ala Val Cys Leu Leu Thr Asp Lys Phe Ile Met Pro Pro Ile Ser
 835 840 845
 Thr Phe Ala Gly Leu Tyr Phe Val Ala Leu Phe Ser Ser Ile Ile Ala
 850 855 860
 Thr Gly Ile Leu Glu Leu Lys Trp Ser Gly Val Ser Ile Glu Glu Trp
 865 870 875 880
 Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu
 885 890 895
 Phe Ala Val Ile Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr
 900 905 910
 Asn Phe Thr Val Thr Ser Lys Ala Thr Asp Asp Glu Glu Phe Gly Glu
 915 920 925
 Leu Tyr Thr Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Ile
 930 935 940
 Leu Ile Ile Asn Ile Val Gly Val Val Ala Gly Ile Ser Asp Ala Ile
 945 950 955 960
 Asn Asn Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe
 965 970 975
 Ser Phe Trp Val Ile Val His Leu Tyr Pro Phe Leu Lys Gly Leu Met
 980 985 990

DRAFT GENOME

Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Val Ile Trp Ser Val Leu
995 1000 1005

Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Val
1010 1015 1020

Leu Lys Thr Lys Gly Pro Asp Thr Lys Leu Cys Gly Ile Asn Cys
1025 1030 1035

<210> 15
<211> 2125
<212> DNA
<213> Glycine max

<400> 15

gccaaggctc	agaagatgcc	agaggaaggt	tggacaatgc	aggatggaac	tccttggcct	60
ggaaataatc	ctagggatca	tccggaatg	attcaggtgt	tttaggtca	tagtgggggg	120
ctggatacac	atggaaatga	gctgcctaga	cttggttatg	tttcgtga	gaagcgacca	180
ggcttccaac	atcacaagaa	ggctggagct	atgaatgctt	tgattcgt	ttctgctgtc	240
ttgaccaatg	gtgcataatct	tctgaatgtg	gattgtgatc	actattcaa	taatagcaaa	300
gccctcaaag	aagccatgtg	tttcatgatg	gatcctgtc	ttggaaagaa	gacatgctat	360
gttcaatttc	ctcagagatt	tgacggcatt	gacttgcacg	atcgatatgc	caatcgcaat	420
attgtgttct	ttgatatcaa	catgaaaggt	caggatgggt	ttcagggccc	agtctatgtg	480
ggaactgggt	gttgttcaa	taggaagct	ttgtatgggt	atgatcctgt	tttgactgag	540
gaagatttgg	aacctaacat	tattgtaaag	agttgttgcg	gttctagaaa	gaagggaaag	600
ggtggcaata	agaagtacag	tgacaagaag	aaggcgatgg	gaagaactga	atccactgta	660
cccatattta	atatggaaag	catagaggag	ggtgttgaag	tttatgtga	tcaaaggaca	720
ctacttatgt	ctcaaaaagag	cttggagaag	cgccccggc	agtctccagt	ttttattgtct	780
gccacttca	tggagcaggg	tggcattcca	ccttcaacga	accctgcaac	tcttcttaag	840
gaagcaatcc	atgttatca	ctgtgttac	gaagacaaga	cagaatgggg	caaagagatt	900
ggatggatct	atggctctgt	gacagaagat	atcttgcactg	gttcaagat	gcatgctcgt	960
ggttggattt	ccatctattt	catgcaccc	cgccccagcat	ttaagggttc	tgctcctatc	1020
aatcttctg	atcgctctaa	tcaggtgctt	cggtggggc	tgggtcaat	tgagatcttt	1080
ctaagcaggc	attgtccctt	gtggtatggc	tacaatggg	agttgaagcc	tctgatgagg	1140
cttgcttata	ttaacaccat	tgtctacccg	tttacctcaa	tcccattgtat	tgcttactgt	1200
acgcttctg	cattttgtct	tctcacaat	aaatttatta	tccctgagat	aagcaacttt	1260
gccagtatgt	ggttcttct	tctcttgc	tccattttta	ccacttcaat	tctttagctt	1320
aggtggagt	gggtcagtat	agaagactgg	tggagaaatg	aacagttctg	ggttacgtt	1380
gggacatctg	cgcacatctt	tgctgttcc	caggggcttc	taaaagtgt	tgctgggatc	1440
gatacaaatt	ttactgttac	atcgaaggca	tcggacgagg	atggggactt	tgccgagctt	1500
tatgtttta	aatggacatc	acttctcatc	cctcctacaa	cagtcttat	tgtgaatttg	1560
gttgggattt	tggctgggt	atcctatgcc	ataaacatgt	gttaccatgc	ttgggggtcca	1620
ctatttggca	actgtttctt	tgctatctgg	gtcattgcc	atctatacc	attcttgaag	1680
ggtctcttgg	gcaggcaaaa	tcgtacccca	accattgtt	ttgtttggc	cgttcttctt	1740
gcttcaatat	tctccttgc	gtgggtgagg	attgatccct	tcacccctga	ctccaacaaa	1800
ttaaccaat	gtcaatgtgg	catcaactgt	tagttctt	gtatgattca	ttttgtgtt	1860
ttattccctt	ttgcttggag	atacacaagg	ttgctgtcgt	gtatatacg	agaattttca	1920
gcctatcaaa	gttgtctgg	ggattgaacc	cctgaaatag	atggaaatgt	accctctctg	1980
tttctattat	ttatctacat	gttccttaca	agaatagtca	gtagtaatgt	tgaggtgtat	2040
gttatatttt	ttccccacag	aatataaatt	tgttcatgcg	aatatttaat	gaaagccaaac	2100
aaggtccctgt	gtgttttgc	tctt				2125

<210> 16
<211> 610
<212> PRT
<213> Glycine max

DQ902222-ZYXVWU

<400> 16
Ala Lys Ala Gln Lys Met Pro Glu Glu Gly Trp Thr Met Gln Asp Gly
1 5 10 15

Thr Pro Trp Pro Gly Asn Asn Pro Arg Asp His Pro Gly Met Ile Gln
20 25 30

Val Phe Leu Gly His Ser Gly Gly Leu Asp Thr Asp Gly Asn Glu Leu
35 40 45

Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln His
50 55 60

His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val Ser Ala Val
65 70 75 80

Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp His Tyr Phe
85 90 95

Asn Asn Ser Lys Ala Leu Lys Glu Ala Met Cys Phe Met Met Asp Pro
100 105 110

Val Leu Gly Lys Lys Thr Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp
115 120 125

Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile Val Phe Phe
130 135 140

Asp Ile Asn Met Lys Gly Gln Asp Gly Val Gln Gly Pro Val Tyr Val
145 150 155 160

Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly Tyr Asp Pro
165 170 175

Val Leu Thr Glu Glu Asp Leu Glu Pro Asn Ile Ile Val Lys Ser Cys
180 185 190

Cys Gly Ser Arg Lys Lys Gly Lys Gly Asn Lys Lys Tyr Ser Asp
195 200 205

Lys Lys Lys Ala Met Gly Arg Thr Glu Ser Thr Val Pro Ile Phe Asn
210 215 220

Met Glu Asp Ile Glu Glu Gly Val Glu Gly Tyr Asp Asp Glu Arg Thr
225 230 235 240

Leu Leu Met Ser Gln Lys Ser Leu Glu Lys Arg Phe Gly Gln Ser Pro
245 250 255

Val Phe Ile Ala Ala Thr Phe Met Glu Gln Gly Gly Ile Pro Pro Ser
260 265 270

Thr Asn Pro Ala Thr Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys
275 280 285

Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr
290 295 300

Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg
305 310 315 320

Gly Trp Ile Ser Ile Tyr Cys Met Pro Pro Arg Pro Ala Phe Lys Gly
 325 330 335

 Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp
 340 345 350

 Ala Leu Gly Ser Ile Glu Ile Phe Leu Ser Arg His Cys Pro Leu Trp
 355 360 365

 Tyr Gly Tyr Asn Gly Lys Leu Lys Pro Leu Met Arg Leu Ala Tyr Ile
 370 375 380

 Asn Thr Ile Val Tyr Pro Phe Thr Ser Ile Pro Leu Ile Ala Tyr Cys
 385 390 395 400

 Thr Leu Pro Ala Phe Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Glu
 405 410 415

 Ile Ser Asn Phe Ala Ser Met Trp Phe Ile Leu Leu Phe Val Ser Ile
 420 425 430

 Phe Thr Thr Ser Ile Leu Glu Leu Arg Trp Ser Gly Val Ser Ile Glu
 435 440 445

 Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr Ser Ala
 450 455 460

 His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile
 465 470 475 480

 Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp
 485 490 495

 Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile Pro Pro
 500 505 510

 Thr Thr Val Leu Ile Val Asn Leu Val Gly Ile Val Ala Gly Val Ser
 515 520 525

 Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys
 530 535 540

 Leu Phe Phe Ala Ile Trp Val Ile Ala His Leu Tyr Pro Phe Leu Lys
 545 550 555 560

 Gly Leu Leu Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile Val Trp
 565 570 575

 Ser Val Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp
 580 585 590

 Pro Phe Thr Ser Asp Ser Asn Lys Leu Thr Asn Gly Gln Cys Gly Ile
 595 600 605

 Asn Cys
 610

 <210> 17
 <211> 2890

© 2009 by S. A. Parker

<212> DNA

<213> Glycine max

<400> 17

gcacgagctc caccaggat atgatgcata tggcttgtgg ttgacatcg tcacatgtga 60
aatatgttt gctgtatcat ggataatgga tcagttcca aaatggtacc caatacaagcg 120
agaaaacatac ctgtatcgtc tgcactcgag gtatgaaaaaa gaagggaaagc catctgagtt 180
gtccagtgta gacgtctttg tcagttactgt tgatcccatt aaggaacctc cactgattac 240
agcaaacact gtttatctta tccttgctgt tgattatcca gttgataaag ttgcatgcta 300
tgtctcagat gatggtgctg ctatgcttac ttttgaagca ctgtctgaga catctgaatt 360
tgcttaggaga tgggttccat tttgttaagaa atacaatatt gagccccggg caccagaatg 420
gtacttttgtt cagaagatgg actatctgaa aaataaagta caccagcat ttgtcaggga 480
aaggagagca atgaagaggg attatgaaga atttaaggtg aggattaaca gtttgggtggc 540
aacagcacaa aagggttctgt aggtatggatg gaccatgcaa gatgggactc cttggcctgg 600
aaataatgtg agggatcatc ctggcatgat tcaggtcttc cttgggcagg atgggtttcg 660
tgatgtgaa gggaaatgagc taccccgctt ggtctacgtt tctagagaaa agaggccagg 720
gtttgatcac cacaaaaaagg ctggtgcaat gaatgctctg gtacggcctt cagcaattat 780
caactatgca ccctatcttc tgaatgttga ttgtatcac tacattaaca atagcaaggc 840
acttagagaa gctatgtt ttatgttga tcctcaacta gggaaaaagg tttgctatgt 900
gcaatttcct cagcgatttg atgaaatttga tagacatgat agatattcaa acagaaatgt 960
tgtatttttc gatattaaca tggaaaggatt ggatgggata caaggtccaa tatatgtcgg 1020
aactggatgt gtttcagaa ggtacgcact ttatggatat gatgcacctg ccaagaagaa 1080
accaccggc aaaacttgcata ctgttggcc aaagtggtgc tgcctatgtt gtggctctag 1140
aaagaaaaag aatgccaata gtaagaagga gaaaaagagg aaggtgaagc acagtgaagc 1200
atcaaagcag atacatgcac ttgaaaatat tgaggcgggg aatgaaggaa ccaacaatgaa 1260
gaagacatcc aatctgactc aaacaaagtt ggagaagagg tttggacagt ctccagttt 1320
tgtagcctcc acacttttgg atgatggtgg agttccacat ggcgtgagtc ctgcatact 1380
tttaaaagaa gccatccagg tcatacggtt tggttatgaa gacaaaacag aatggggaaa 1440
agaagttggg tggatatatg gttctgtgac agaggatatc ttgactggat taaaatgtca 1500
ttgccatggg tggcggtctg tggattgtcat tcctaagcgg cctgcattta aggggtctgc 1560
gcctatcaac ctttcagatc gtctgcacca agttcttcgg tgggtcttg ggtctgttga 1620
gattttttc agcagacatt gtccaaatctg gtatggctat ggtgggtggat tggaaattgtt 1680
ggaacgattt tcctacattt actcggctgtt atatccctgg acttccctcc cattgcttgt 1740
ctactgtact ctaccagcca tatgccttct gactggaaaaa tttatcgatcc cggagattag 1800
caactatgcc agtcttgcata tcataggccct cttcatatcc attgcagcaa ctggcatcct 1860
tgagatgcaat tggggcggtt ttagcataga cgactggtgg aggaacgaac agttttgggt 1920
gatcggaggt gtttcttccc atctatttgc cttatattcag gtttactgtt aggtcttggc 1980
tgggtgttac acaaacttca ctgtgacctc aaaaggcagca gatgtatggag aattctcaga 2040
actctacata ttcaagtggc catcaactt gatcccttca atgactttac ttatcatgaa 2100
tattgtcggg gtgggtgtcg ggtatcaga tggcatcaac aatggttatg actcatgggg 2160
acctctctt ggttagattgt tctttgcatt gtgggtgttgc ctccatctt accccttctt 2220
gaaggggttgc ctggaaaaac aagatagaat gccaaccatt atattggttt ggtcaatcct 2280
tctggcctcc atcttgcactc tcatagggtt cagaatttac ccgtttgtgtt caagagacgg 2340
ccccgtgtta gaaatttgcata gatttgcattt ggttttttgc tgggtgttgc ttatcatgaa 2400
aagaagggtt agttatattt cagctacact gcaatgttgc tggatggatcc agccagcaca 2460
tgcttcacaa agttgcacca attttgcattt ggttttttgc tggatggatcc agccagcaca 2520
taaagagagg aagggggaggg ggctgacaca ttgttacccat gtaatagggt tttttcattt 2580
attctttgtat tatattttctt gtttttttgc tggatggatcc tttttcattt tttttcattt 2640
taagaaagag gcattgtatcataaaatttccat ttttttttgc tggatggatcc ctttttttgc 2700
aagaaatttac ttgttcatat ttttttttgc tggatggatcc ttttttttgc tggatggatcc 2760
taccgtcaaa actatggata ttcttgcattt ttttttttgc tggatggatcc ttttttttgc 2820
caactcaggaa ctttttttgc tggatggatcc ttttttttgc tggatggatcc ttttttttgc 2880
aaaaaaaaaaaa 2890

<210> 18

<211> 793

<212> PRT

<213> Glycine max

TOP SECRET//NOFORN

<400> 18
His Glu Leu His Pro Val Asn Asp Ala Tyr Gly Leu Trp Leu Thr Ser
1 5 10 15

Val Ile Cys Glu Ile Trp Phe Ala Val Ser Trp Ile Met Asp Gln Phe
20 25 30

Pro Lys Trp Tyr Pro Ile Gln Arg Glu Thr Tyr Leu Asp Arg Leu Ser
35 40 45

Leu Arg Tyr Glu Lys Glu Gly Lys Pro Ser Glu Leu Ser Ser Val Asp
50 55 60

Val Phe Val Ser Thr Val Asp Pro Met Lys Glu Pro Pro Leu Ile Thr
65 70 75 80

Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys
85 90 95

Val Ala Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu
100 105 110

Ala Leu Ser Glu Thr Ser Glu Phe Ala Arg Arg Trp Val Pro Phe Cys
115 120 125

Lys Lys Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Gly Gln
130 135 140

Lys Met Asp Tyr Leu Lys Asn Lys Val His Pro Ala Phe Val Arg Glu
145 150 155 160

Arg Arg Ala Met Lys Arg Asp Tyr Glu Glu Phe Lys Val Arg Ile Asn
165 170 175

Ser Leu Val Ala Thr Ala Gln Lys Val Pro Glu Asp Gly Trp Thr Met
180 185 190

Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Val Arg Asp His Pro Gly
195 200 205

Met Ile Gln Val Phe Leu Gly Gln Asp Gly Val Arg Asp Val Glu Gly
210 215 220

Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly
225 230 235 240

Phe Asp His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Ala
245 250 255

Ser Ala Ile Ile Thr Asn Ala Pro Tyr Leu Leu Asn Val Asp Cys Asp
260 265 270

His Tyr Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met
275 280 285

Met Asp Pro Gln Leu Gly Lys Lys Val Cys Tyr Val Gln Phe Pro Gln
290 295 300

Arg Phe Asp Gly Ile Asp Arg His Asp Arg Tyr Ser Asn Arg Asn Val
305 310 315 320

Val Phe Phe Asp Ile Asn Met Lys Gly Leu Asp Gly Ile Gln Gly Pro
 325 330 335

 Ile Tyr Val Gly Thr Gly Cys Val Phe Arg Arg Tyr Ala Leu Tyr Gly
 340 345 350

 Tyr Asp Ala Pro Ala Lys Lys Pro Pro Ser Lys Thr Cys Asn Cys
 355 360 365

 Trp Pro Lys Trp Cys Cys Leu Cys Cys Gly Ser Arg Lys Lys Lys Asn
 370 375 380

 Ala Asn Ser Lys Lys Glu Lys Lys Arg Lys Val Lys His Ser Glu Ala
 385 390 395 400

 Ser Lys Gln Ile His Ala Leu Glu Asn Ile Glu Ala Gly Asn Glu Gly
 405 410 415

 Thr Asn Asn Glu Lys Thr Ser Asn Leu Thr Gln Thr Lys Leu Glu Lys
 420 425 430

 Arg Phe Gly Gln Ser Pro Val Phe Val Ala Ser Thr Leu Leu Asp Asp
 435 440 445

 Gly Gly Val Pro His Gly Val Ser Pro Ala Ser Leu Leu Lys Glu Ala
 450 455 460

 Ile Gln Val Ile Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys
 465 470 475 480

 Glu Val Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly
 485 490 495

 Phe Lys Met His Cys His Gly Trp Arg Ser Val Tyr Cys Ile Pro Lys
 500 505 510

 Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu
 515 520 525

 His Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Phe Phe Ser
 530 535 540

 Arg His Cys Pro Ile Trp Tyr Gly Tyr Gly Gly Leu Lys Leu Leu
 545 550 555 560

 Glu Arg Phe Ser Tyr Ile Asn Ser Val Val Tyr Pro Trp Thr Ser Leu
 565 570 575

 Pro Leu Leu Val Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly
 580 585 590

 Lys Phe Ile Val Pro Glu Ile Ser Asn Tyr Ala Ser Leu Val Phe Met
 595 600 605

 Ala Leu Phe Ile Ser Ile Ala Ala Thr Gly Ile Leu Glu Met Gln Trp
 610 615 620

 Gly Gly Val Ser Ile Asp Asp Trp Trp Arg Asn Glu Gln Phe Trp Val
 625 630 635 640

Ile	Gly	Gly	Val	Ser	Ser	His	Leu	Phe	Ala	Leu	Phe	Gln	Gly	Leu	Leu
						645			650				655		
Lys	Val	Leu	Ala	Gly	Val	Asn	Thr	Asn	Phe	Thr	Val	Thr	Ser	Lys	Ala
						660			665				670		
Ala	Asp	Asp	Gly	Glu	Phe	Ser	Glu	Leu	Tyr	Ile	Phe	Lys	Trp	Thr	Ser
						675			680			685			
Leu	Leu	Ile	Pro	Pro	Met	Thr	Leu	Leu	Ile	Met	Asn	Ile	Val	Gly	Val
						690			695			700			
Val	Val	Gly	Ile	Ser	Asp	Ala	Ile	Asn	Asn	Gly	Tyr	Asp	Ser	Trp	Gly
						705			710			715			720
Pro	Leu	Phe	Gly	Arg	Leu	Phe	Phe	Ala	Leu	Trp	Val	Ile	Leu	His	Leu
						725			730			735			
Tyr	Pro	Phe	Leu	Lys	Gly	Leu	Leu	Gly	Lys	Gln	Asp	Arg	Met	Pro	Thr
						740			745				750		
Ile	Ile	Leu	Val	Trp	Ser	Ile	Leu	Leu	Ala	Ser	Ile	Leu	Thr	Leu	Met
						755			760			765			
Trp	Val	Arg	Ile	Asn	Pro	Phe	Val	Ser	Arg	Asp	Gly	Pro	Val	Leu	Glu
						770			775			780			
Ile	Cys	Gly	Leu	Asn	Cys	Asp	Glu	Ser							
						785			790						

```
<210> 19
<211> 1733
<212> DNA
<213> Triticum aestivum
```

<220>
<221> unsure
<222> (262)

catctgtttg ccgtcttca gggcttctg aaggcttg caggtatcga caccaacttc 1140
actgtcacct caaaggctaa tgatgaagaa ggcgacttg ctgagctcta catgttcaag 1200
tggacgacgc ttcttatccc tccgacgacc attttgcata ttaacatggt cggtgtcggt 1260
gctggcacct cctacgcccc caacagtggt taccaatcat gggggccgct ctttggaaag 1320
ctcttctttg cttctgggt gattgtcac ttataccat tcctcaaggg tcttatggc 1380
aggcaaaacc gcacaccgac gattgtcatc gtctgggctg tcctcctcgc ttcttatctc 1440
tccttgcgtg ggggtcggt tgatccattc actaccgc tcgctggccc aaatatccaa 1500
acctgtggca tcaactgcta ggaaagtggg agtttgcata gacagaaaat ataacagtga 1560
tcgagcgacc acctgtggag ccagagaata tttatgtgg ggttgtaat tactacgtt 1620
gagaaagttg tcaaattga gaaaacacat ttgtaaatag atgtaaataga ctatctaccg 1680
tttcatgag gttaagctct tcttttgg aaaaaaaaaaaa aaaaaaaaaaaa aaa 1733

<210> 20
<211> 506
<212> PRT
<213> Triticum aestivum

<220>
<221> UNSURE
<222> (88)

<400> 20
Glu Ala Met Cys Phe Leu Met Asp Pro Asn Leu Gly Pro Gln Val Cys
1 5 10 15

Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp Arg
20 25 30

Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu
35 40 45

Asp Gly Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn
50 55 60

Arg Thr Ala Ile Tyr Gly Tyr Glu Pro Pro Ile Lys Ala Lys Lys Pro
65 70 75 80

Gly Phe Leu Ala Ser Leu Cys Xaa Gly Lys Lys Lys Ala Ser Lys Ser
85 90 95

Lys Lys Arg Ser Ser Asp Lys Lys Ser Asn Lys His Val Asp Ser
100 105 110

Ser Val Pro Val Phe Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly
115 120 125

Ala Gly Phe Asp Asp Glu Lys Ser Val Leu Met Ser Gln Met Ser Leu
130 135 140

Glu Lys Arg Phe Gly Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met
145 150 155 160

Glu Tyr Gly Gly Val Pro Gln Ser Ser Thr Pro Glu Ser Leu Leu Lys
165 170 175

Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys Ser Glu Trp
180 185 190

Gly Thr Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu
 195 200 205
 Thr Gly Phe Lys Met His Ala Arg Gly Trp Arg Ser Ile Tyr Cys Met
 210 215 220
 Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp
 225 230 235 240
 Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu
 245 250 255
 Phe Ser Arg His Cys Pro Leu Trp Tyr Gly Tyr Gly Arg Leu Lys
 260 265 270
 Phe Leu Glu Arg Phe Ala Tyr Ile Asn Thr Thr Ile Tyr Pro Leu Thr
 275 280 285
 Ser Leu Pro Leu Leu Val Tyr Cys Ile Leu Pro Ala Ile Cys Leu Leu
 290 295 300
 Thr Gly Lys Phe Ile Met Pro Glu Ile Ser Asn Leu Ala Ser Ile Trp
 305 310 315 320
 Phe Ile Ala Leu Phe Leu Ser Ile Phe Ala Thr Gly Ile Leu Glu Met
 325 330 335
 Arg Trp Ser Gly Val Gly Ile Asp Glu Trp Trp Arg Asn Glu Gln Phe
 340 345 350
 Trp Val Ile Gly Gly Ile Ser Ala His Leu Phe Ala Val Phe Gln Gly
 355 360 365
 Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser
 370 375 380
 Lys Ala Asn Asp Glu Glu Gly Asp Phe Ala Glu Leu Tyr Met Phe Lys
 385 390 395 400
 Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Ile Leu Ile Ile Asn Met
 405 410 415
 Val Gly Val Val Ala Gly Thr Ser Tyr Ala Ile Asn Ser Gly Tyr Gln
 420 425 430
 Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile
 435 440 445
 Val His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg
 450 455 460
 Thr Pro Thr Ile Val Ile Val Trp Ala Val Leu Leu Ala Ser Ile Phe
 465 470 475 480
 Ser Leu Leu Trp Val Arg Val Asp Pro Phe Thr Thr Arg Leu Ala Gly
 485 490 495
 Pro Asn Ile Gln Thr Cys Gly Ile Asn Cys
 500 505

<210> 21
 <211> 1029
 <212> DNA
 <213> Triticum aestivum

<400> 21
 gcacgagccg ctccctcacca acggccagat ggttgatgac atcccgcgg agcagcacgc 60
 gctcgccg tcctacatga gcggccggcgg cggcgggggc aagaggatcc acccgctccc 120
 tttcgagat cccaaccttc cagtgcacc accatgatcc gaccgtcca agatctggc 180
 cgccctacgga tatggcagcg tggccctggaa ggagagaatg gagggcttgg agcagaagca 240
 ggagcgcccg cagcatgtca ggagcgaggg tggcggtat tggatggcg acgatgcaga 300
 tctgccacta atggatgaag ctaggcagcc attgtccaga aaagtcccta tatcatcaag 360
 ccgaattaat ccctacagga tgattatcgat tatccgggtt gtggttttgg gtttcttctt 420
 ccactaccga gtgatgcata cggcgaaaga tgcatttgca ttgtggctca tatctgtat 480
 ctgtgaaatc tggtttgcga tgcctgtat tcttgcata ttcccaaagt gtttccaat 540
 cgagagagag acttacctgg accgtttgtc actaagggtt gacaaggaag gtcaaccctc 600
 tcagcttgcct ccaatcgact tctttgtcag tacgggtat cccacaaaagg aacccctt 660
 ggtcacacgca aacactgtcc ttccatcct ttctgtggat tatccgggtt agaaggctc 720
 ctgctatgtt tctgatgatg gtgctgcaat gtttgcattt gaagcattgt ctgaaacatc 780
 tgaatttgca aagaaatggg ttcccttcag caaaaaagtt aatatcgagc ctcgtgctcc 840
 tgagtggtaa ttccaaacaga agatagacta cctgaaagac aaggttgctg cttcatttgt 900
 tagggagagg agggcgatga agagagaata cgaggaattc aaggtaagga tcaatgcctt 960
 ggttgcaaaa gcccaaaagg ttccctgagga aggatggaca atgcaagatg gaagccctg 1020
 gcctggaaa 1029

<210> 22
 <211> 340
 <212> PRT
 <213> Triticum aestivum

<400> 22
 Pro Leu Leu Thr Asn Gly Gln Met Val Asp Asp Ile Pro Pro Glu Gln
 1 5 10 15

His Ala Leu Val Pro Ser Tyr Met Ser Gly Gly Gly Gly Gly Lys
 20 25 30

Arg Ile His Pro Leu Pro Phe Ala Asp Pro Asn Leu Pro Val Gln Pro
 35 40 45

Arg Ser Met Asp Pro Ser Lys Asp Leu Ala Ala Tyr Gly Tyr Gly Ser
 50 55 60

Val Ala Trp Lys Glu Arg Met Glu Gly Trp Lys Gln Lys Gln Glu Arg
 65 70 75 80

Leu Gln His Val Arg Ser Glu Gly Gly Asp Trp Asp Gly Asp Asp
 85 90 95

Ala Asp Leu Pro Leu Met Asp Glu Ala Arg Gln Pro Leu Ser Arg Lys
 100 105 110

Val Pro Ile Ser Ser Ser Arg Ile Asn Pro Tyr Arg Met Ile Ile Val
 115 120 125

Ile Arg Leu Val Val Leu Gly Phe Phe Phe His Tyr Arg Val Met His
 130 135 140

Pro Ala Lys Asp Ala Phe Ala Leu Trp Leu Ile Ser Val Ile Cys Glu
 145 150 155 160

TOSONV01200660

Ile	Trp	Phe	Ala	Met	Ser	Cys	Ile	Leu	Asp	Gln	Phe	Pro	Lys	Trp	Phe
165									170					175	
Pro	Ile	Glu	Arg	Glu	Thr	Tyr	Leu	Asp	Arg	Leu	Ser	Leu	Arg	Phe	Asp
180								185					190		
Lys	Glu	Gly	Gln	Pro	Ser	Gln	Leu	Ala	Pro	Ile	Asp	Phe	Phe	Val	Ser
195							200						205		
Thr	Val	Asp	Pro	Thr	Lys	Glu	Pro	Pro	Leu	Val	Thr	Ala	Asn	Thr	Val
210							215					220			
Leu	Ser	Ile	Leu	Ser	Val	Asp	Tyr	Pro	Val	Glu	Lys	Val	Ser	Cys	Tyr
225							230				235			240	
Val	Ser	Asp	Asp	Gly	Ala	Ala	Met	Leu	Thr	Phe	Glu	Ala	Leu	Ser	Glu
					245				250				255		
Thr	Ser	Glu	Phe	Ala	Lys	Lys	Trp	Val	Pro	Phe	Ser	Lys	Lys	Phe	Asn
					260				265				270		
Ile	Glu	Pro	Arg	Ala	Pro	Glu	Trp	Tyr	Phe	Gln	Gln	Lys	Ile	Asp	Tyr
275							280					285			
Leu	Lys	Asp	Lys	Val	Ala	Ala	Ser	Phe	Val	Arg	Glu	Arg	Arg	Ala	Met
290							295					300			
Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys	Val	Arg	Ile	Asn	Ala	Leu	Val	Ala
305							310				315			320	
Lys	Ala	Gln	Lys	Val	Pro	Glu	Glu	Gly	Trp	Thr	Met	Gln	Asp	Gly	Ser
					325				330				335		
Pro	Trp	Pro	Gly												
			340												

<210> 23
<211> 2663
<212> DNA
<213> Picramnia pentandra

<400> 23

gcacgaggaa	agaggggaag	ccatctgagc	tagctggctt	agacatattt	gtcagtacgg	60
tggatcctat	gaaaagaacct	ccacttatca	ctgcaaatac	tgtgctatcc	atccttgca	120
ttgattatcc	agttgataaa	gttacatgct	acgtgtcaga	tgatggct	gccatgctta	180
ctttgaagc	actttctgaa	acatctgaat	ttgcacgaaa	atgggtccct	ttctgttaaga	240
agtttagcat	tgaggcctcg	gcaccagaat	gttatttctc	tcagaagatg	gactatttga	300
agaacaaagt	acacccatca	tttgttaggg	aaagacgtgc	tatgaagaga	gaatatgaag	360
tattcaaagt	tcggataaat	ggtttggtt	ccatggcaca	aaaggccc	gaggatgg	420
ggacgatgca	ggatgggact	ccttggcctg	gaaataatgt	gcgagaccat	cctggcatga	480
ttcagggttt	ccttggcac	aatgggttcc	gtgatgttga	aggaaacgag	ttgcctcg	540
tgatatatgt	ttctcgtgag	aagagacctg	gctttgagca	ccataaaaag	gctggtgca	600
tgaattctt	ggtacgggtc	tccgcggta	tctcaaatgc	accctatata	ctaaacgtt	660
actgtgatca	ttacatcaac	aatagcaaag	cactgagaga	agccatgtgt	ttcatgttg	720
atccaacatc	gggaaagaaa	ttatgtatg	tgcagttcc	tcaaagattt	gatggcattt	780
atcgccatga	tcgatattcc	aaccggaatg	ttgtattctt	tgatataat	atgaaaggat	840
tagatggcat	acaagggcct	atatatgtt	gaacgggatg	tgtttcaga	agagtagcac	900
tttatggcta	tgatgcacca	gtcactaaga	agtccccggg	aaaagttgt	aactgttggc	960

ctaaatggtt gtgctgctgt tgcgttcca gaaagaaca gaaatcgaaa ccaaagaagg 1020
 agaagaagaa gtctaaaaat aggaaagcat caaagcagat acatgctctt gaaaatattg 1080
 aagaaggtat gggaggattt aactctgaga aatcatgtga gacaaccca ctgaaattgg 1140
 agaagaagtt tggacagtct ccagtgttcg tggcttctac tcttctagaa gatggtgagg 1200
 tccctcaaga tgcaactcct gcagcactac taaaagaagc catacaggc atcagctgt 1260
 gttatgaaga taaaacagaa tggggaaagg aagttggttt gatatatggc tctgtaacgg 1320
 aggatattct gactggattt aagatgcact gccatggatg gcggctgtg tactgcattc 1380
 ctgcacgccc cgcatattaag gggtcagctc ccatcaacct ttcatgcgtt ctacatcagg 1440
 ttcttcgggtt ggcccttggg tctgtggaga ttttctttag cagacattgtt ccactctgtt 1500
 atggctatgg tggtggttta aaatggttt aagcggtttc ctatgtcgt tcgggtgtt 1560
 atccttggac ctccattccct ttgctgtttt actgcacact gccagccatt tgccttctt 1620
 ctggaaattt cattgttccctt gagattagca actatgcaag catcttggttt atgctccctt 1680
 tcataattttat tgctgcaacc agcattttt agatgcaatg gggtggtgtt ggaatagatg 1740
 attggtgagg aaatgagcaa ttttgggtca ttggagggtt ttcatcacat cttttgtct 1800
 tcttccaagg ttactgaag gttctggctg gtgtgaacac aaacttcact gttacctcta 1860
 aggctgctga tgaaggggat ttctcagagc ttacactt caagtgacca accttattaa 1920
 ttcctccac aacgttggttt atcataaata ttgttgggtt tgggttggc gtctccgatg 1980
 ccatcaataa tggttatgat tcatgggtc ctttgggtt tcggctattt ttgcattct 2040
 gggtcattgtt ccacctctat ctttccca aagggtttgtt tggggaaacaa gatgcacac 2100
 caaccattat tgggtctgg tctattctgc tggcttcaat tctaaccctt ttgtgggtac 2160
 gaataaaatcc atttgtgtcg agagatggcc ctgttggta agtgtgtggg ttaaattgtg 2220
 actaggagac atgaataaaaaa tggttatgat gttttttt ggtcaaaatc cctgatgtct 2280
 gttgtggagc tatggattat gtctattgtat tgcaagtgtat gtttgcaccc atgcattact 2340
 gggaaagatac aattttgtgc aagttttagt gttgggtggg tggtagatatt aagatgagga 2400
 gggttgacac attgtcattt gtttacaga gtttcatta attcttttat tattttttgt 2460
 gggtgttagtt ttttgggttc tttagctttt tcttcagatc tcctgttattt ctaagaaata 2520
 attgagtcat aattttgttcc attgtcaatg tttaggaata atttctcatc tgggtttct 2580
 gctgtttcgtt ctggaaaca tggacgtgtt tgggttctgtt atgaagttac tggaaatatta 2640
 tggtaaaaaa aaaaaaaaaaaa aaa 2663

<210> 24

<211> 740

<212> PRT

<213> Picramnia pentandra

<400> 24

Thr	Arg	Lys	Glu	Gly	Lys	Pro	Ser	Glu	Leu	Ala	Gly	Leu	Asp	Ile	Phe
1															10

Val	Ser	Thr	Val	Asp	Pro	Met	Lys	Glu	Pro	Pro	Leu	Ile	Thr	Ala	Asn
															20
															25
															30

Thr	Val	Leu	Ser	Ile	Leu	Ala	Val	Asp	Tyr	Pro	Val	Asp	Lys	Val	Thr
															35
															40
															45

Cys	Tyr	Val	Ser	Asp	Asp	Gly	Ala	Ala	Met	Leu	Thr	Phe	Glu	Ala	Leu
															50
															55
															60

Ser	Glu	Thr	Ser	Glu	Phe	Ala	Arg	Lys	Trp	Val	Pro	Phe	Cys	Lys	Lys
															65
															70
															75
															80

Phe	Ser	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Trp	Tyr	Phe	Ser	Gln	Lys	Met
															85
															90
															95

Asp	Tyr	Leu	Lys	Asn	Lys	Val	His	Pro	Ser	Phe	Val	Arg	Glu	Arg	Arg
															100
															105
															110

Ala	Met	Lys	Arg	Glu	Tyr	Glu	Val	Phe	Lys	Val	Arg	Ile	Asn	Gly	Leu
															115
															120
															125

TOP SECRET

Val	Ala	Met	Ala	Gln	Lys	Val	Pro	Glu	Asp	Gly	Trp	Thr	Met	Gln	Asp
130						135						140			
Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	Val	Arg	Asp	His	Pro	Gly	Met	Ile
145					150				155					160	
Gln	Val	Phe	Leu	Gly	His	Asn	Gly	Val	Arg	Asp	Val	Glu	Gly	Asn	Glu
					165				170					175	
Leu	Pro	Arg	Leu	Ile	Tyr	Val	Ser	Arg	Glu	Lys	Arg	Pro	Gly	Phe	Glu
					180			185						190	
His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ser	Leu	Val	Arg	Val	Ser	Ala
					195			200					205		
Val	Ile	Ser	Asn	Ala	Pro	Tyr	Ile	Leu	Asn	Val	Asp	Cys	Asp	His	Tyr
					210			215			220				
Ile	Asn	Asn	Ser	Lys	Ala	Leu	Arg	Glu	Ala	Met	Cys	Phe	Met	Met	Asp
					225			230			235			240	
Pro	Thr	Ser	Gly	Lys	Lys	Leu	Cys	Tyr	Val	Gln	Phe	Pro	Gln	Arg	Phe
					245			250					255		
Asp	Gly	Ile	Asp	Arg	His	Asp	Arg	Tyr	Ser	Asn	Arg	Asn	Val	Val	Phe
					260			265					270		
Phe	Asp	Ile	Asn	Met	Lys	Gly	Leu	Asp	Gly	Ile	Gln	Gly	Pro	Ile	Tyr
					275			280			285				
Val	Gly	Thr	Gly	Cys	Val	Phe	Arg	Arg	Val	Ala	Leu	Tyr	Gly	Tyr	Asp
					290			295			300				
Ala	Pro	Val	Thr	Lys	Lys	Ser	Pro	Gly	Lys	Ala	Cys	Asn	Cys	Trp	Pro
					305			310			315			320	
Lys	Trp	Leu	Cys	Cys	Cys	Gly	Ser	Arg	Lys	Asn	Lys	Lys	Ser	Lys	
					325			330					335		
Pro	Lys	Lys	Glu	Lys	Lys	Ser	Lys	Asn	Arg	Glu	Ala	Ser	Lys	Gln	
					340			345					350		
Ile	His	Ala	Leu	Glu	Asn	Ile	Glu	Glu	Gly	Met	Gly	Gly	Leu	Asn	Ser
					355			360			365				
Glu	Lys	Ser	Cys	Glu	Thr	Thr	Pro	Leu	Lys	Leu	Glu	Lys	Lys	Phe	Gly
					370			375			380				
Gln	Ser	Pro	Val	Phe	Val	Ala	Ser	Thr	Leu	Leu	Glu	Asp	Gly	Gly	Val
					385			390			395			400	
Pro	Gln	Asp	Ala	Thr	Pro	Ala	Ala	Leu	Leu	Lys	Glu	Ala	Ile	Gln	Val
					405			410					415		
Ile	Ser	Cys	Gly	Tyr	Glu	Asp	Lys	Thr	Glu	Trp	Gly	Lys	Glu	Val	Gly
					420			425					430		
Trp	Ile	Tyr	Gly	Ser	Val	Thr	Glu	Asp	Ile	Leu	Thr	Gly	Phe	Lys	Met
					435			440			445				

TOP SECRET//NOFORN

His	Cys	His	Gly	Trp	Arg	Ser	Val	Tyr	Cys	Met	Pro	Ala	Arg	Pro	Ala
450															460
Phe	Lys	Gly	Ser	Ala	Pro	Ile	Asn	Leu	Ser	Asp	Arg	Leu	His	Gln	Val
465															480
Leu	Arg	Trp	Ala	Leu	Gly	Ser	Val	Glu	Ile	Phe	Leu	Ser	Arg	His	Cys
															495
485															
Pro	Leu	Trp	Tyr	Gly	Tyr	Gly	Gly	Leu	Lys	Trp	Leu	Glu	Arg	Phe	
															510
500															
Ser	Tyr	Val	Ser	Ser	Val	Val	Tyr	Pro	Trp	Thr	Ser	Ile	Pro	Leu	Leu
515															
Val	Tyr	Cys	Thr	Leu	Pro	Ala	Ile	Cys	Leu	Leu	Thr	Gly	Lys	Phe	Ile
															540
530															
Val	Pro	Glu	Ile	Ser	Asn	Tyr	Ala	Ser	Ile	Leu	Phe	Met	Leu	Leu	Phe
															560
545															
Ile	Phe	Ile	Ala	Ala	Thr	Ser	Ile	Leu	Glu	Met	Gln	Trp	Gly	Gly	Val
															575
565															
Gly	Ile	Asp	Asp	Trp	Trp	Arg	Asn	Glu	Gln	Phe	Trp	Val	Ile	Gly	Gly
															590
580															
Val	Ser	Ser	His	Leu	Phe	Ala	Leu	Phe	Gln	Gly	Leu	Leu	Lys	Val	Leu
															605
595															
Ala	Gly	Val	Asn	Thr	Asn	Phe	Thr	Val	Thr	Ser	Lys	Ala	Ala	Asp	Glu
															620
610															
Gly	Asp	Phe	Ser	Glu	Leu	Tyr	Leu	Phe	Lys	Trp	Thr	Thr	Leu	Leu	Ile
															640
625															
Pro	Pro	Thr	Thr	Leu	Leu	Ile	Ile	Asn	Ile	Val	Gly	Val	Val	Val	Gly
															655
645															
Val	Ser	Asp	Ala	Ile	Asn	Asn	Gly	Tyr	Asp	Ser	Trp	Gly	Pro	Leu	Phe
															670
660															
Gly	Arg	Leu	Phe	Phe	Ala	Phe	Trp	Val	Ile	Val	His	Leu	Tyr	Pro	Phe
															685
675															
Leu	Lys	Gly	Leu	Leu	Gly	Lys	Gln	Asp	Arg	Thr	Pro	Thr	Ile	Ile	Val
															700
690															
Val	Trp	Ser	Ile	Leu	Leu	Ala	Ser	Ile	Leu	Thr	Leu	Leu	Trp	Val	Arg
															720
705															
Ile	Asn	Pro	Phe	Val	Ser	Arg	Asp	Gly	Pro	Val	Leu	Glu	Val	Cys	Gly
															735
725															
Leu	Asn	Cys	Asp												
															740

DRAFT

```

<210> 25
<211> 3563
<212> DNA
<213> Impatiens balsamia

<400> 25
gcacgagagg caaacgccgg actagtcgcc ggatcttaca agcggAACGA gcttgtccga 60
attcgccacg attcatgg cgcccAGCCG aAGCCCCTAA aAGGGCTAA CGGACAGATA 120
tgtcagatgt gCGGTGACAC AGTCGGAAAAA TCAAGCCACCG GCGACACTT CGTTGCCTGT 180
aatgaatgtg gATTCCCCGT TTGCCGGCCT TGTACGAGT ACGAAAGGAA AGATGGAAC 240
caatgtgcc cTCAGTGCAA GACCAGATAC AAAAGACAGA AAGGGAGTCC TAGAGTTGAA 300
ggagatgaag aAGAGGAGGA TGTGGATGAT TTGGAAAACG AGTTCAATT TAATCGGTAAA 360
gggaagaacc aGAAGAAAGGT AACCAACGGCA AGGCAGGCCAT GGCAGGGAGA TCAGCAGGAT 420
attgagctct ctGTTTCACTC ATCTAGGCAT GATGAATCCC AACAACCTGT ACCTCTTC 480
actcacgggc ACTCGGTATC GGGCGAAATT CCCACTCCC ATAATCATT CATAAGGACT 540
acatcaggTC CCATAGGCC TGTGGAAAAAA TCCATCCCT ATATCGATCC CAGGCAGCCA 600
gttgctgtga gaataatgtg tgACCCCTTC aAGGACTTGA ACTCGTACGG GCTTGGCAAT 660
gtggatgtga aggaaagggtg tGAAGGTTGG AAACCTTAAGC AGGAGAAAAAA TATGGTGC 720
atgaccagta gATATCCTGA AGGGAAAGGA GATACTGAAG GTACGGGATC AAATGGGGAG 780
gaacctcaaa tGGCTGCCGA CGATATCCGA CAACCCATGA GCCGAATCGT GCCCATTTC 840
tcgacgcacc tcACTCCCTA CAGAGTGGTT ATCATACTTC GGTTAATTAT CCTCGGTT 900
ttcttgcaat accgttgtac tCATCCAGTG AAAGATGCTT ATCCATTATG GCTTACCTG 960
gttatttgtg aAGTTTGGTT TGCAATTGTCA TGGCTGCTTG ATCAGTTCCC TAAATGGTC 1020
cctgtgaacc gCGAGACTTA TCTCGACAGA CTGTCCATGA GATTGATAG GGAAGGGAG 1080
ccttcgcaat tGGCGCCAAT TGACGTATT GTTAGTACCG TGGATCCTT GAAAGAGCCA 1140
ccactcgtga cAGCCAACAC GGTTTGTCT ATCCTGGCCG TGGATTACCC TGTGACAAA 1200
gtctcttgct atGTTTCCGA TGACGTTCA GCAATGTTGA CCTTCGAAGC TCTATCCGAG 1260
acagccgagt ttGCTAAAGAA ATGGGCACCC TTCTGTAAAG AACATAGTAT TGAACCTCGG 1320
gcccggcaat ttTATTTCGC TCAAAAAGATT GATTACTTGAG AGGATAAGGT GCAGCCTCT 1380
ttcgtgaagg agCGGAGGGC GATGAAGAGG GAATACGAAG AATTAAAGGT TAGGATTAAT 1440
gcccgggtt cGAAAGCGCA AAAAGTGCCA GAAGAAGGAT GGACATGCA AGATGGAACT 1500
ccatggccgg gAAATAACTC GAGAGATCAT CTCGGAATGA TTCAGGTTT TTTAGGCCAT 1560
agtgggggtt tcgatacggg gggAAATGAG TTACCTCGC TGGTGTACGT TTCTCGTAG 1620
aaacgtcctg gATTTCAGCA TCAACAAGAAA GCGGGGGCAA TGAACGCATT GATTGAGTA 1680
tcggcagtgc tgacAAATGG GGCTTATCTG CTTAACGTGG ATTGTGATCA CTACTTCAC 1740
aacagcaaat gtctAAAAGA GGCAATGTGC TTTATGATGG ATCCAAACCT TGGAAAGAAA 1800
acatgttacg ttCAAGTCCC TCAACGGTTT GATGGTATTG ACTTGCACGA TCGATATGCT 1860
aaccgtaaaca ttgtcttctt CGATATCAAC TTGAAAGGGT TGGACGGCAT TCAGGGCCA 1920
gtttatgtgg gtACCGGTTT TTGTTCAAC AGACAGGCGC TATACTGGTA TGATCCAGTC 1980
ttaacagagg aggatttggg accgaatATC ATCATCAAGA GCTGGTGCAG CTCGAGGAAA 2040
aagggtAAAG gtggcaacAA GAAGTACATT GACA AAAACA GAGCACTAA GCGAACCGAA 2100
tcaaccgcgc ccATTTCAA TATGGAAGAT ATTGAAGAGG GCATTGAAGG TTACGATGAC 2160
gagagatctt ttctcatggc acAGAGTTAC GAAAAGCGGT TCGGTCAATC CCCTGTTCTT 2220
attgctgcca cgttcatggc ACAAGGCGGC CTTCTCCCTT CCACAAACTC TGCAACCTCT 2280
ttgaaAGAAAG CAATCCATGT TATTAGCTGT GGGTACGAGG ACAAGACTGA ATGGGGCAA 2340
gagattggat ggatATATGG ATCTGTAACG GAAGATATCT TGACCGGTT CAAGATGCT 2400
acgagaggat ggATTCAAT CTACTGCATG CCGCCACGCC CTGCCTCAA AGGATCTGCA 2460
cccattaatc ttccggatcg ttGAACCAAG GTCCTTCGAT GGGCTCTGG ATCGATTGAG 2520
attctttgaa gtagacattt cccccATTGG TATGGCTACA GCGGTAGACT CAAGTCTTG 2580
gagagattgg ctttatataa tactattgtt TATCCACTCA CCTCCATTCC TTTACTTGCT 2640
tattgcaccc ttccTGTAT CTGCTTACTC ACCGGAAAAT TCACTGTTCC GGAGATAAGC 2700
aactacgcga gcatctgggt cATTCTTCTG TTCGTGTCTA TTTCTCGAC GGGAAATCTG 2760
gagctaAGAT ggAGCGGGGT TACACTGGAG GACTGGTGA GAAACGAGCA ATTCTGGTA 2820
atcggTGGCA CGTCGGCTCA TCTCTTGCCT GTGTTCCAAG GCCTGCTAAA AGTGTCTGCG 2880
gggatcgaca cgaatttcac CGTCACGTCG AAAGCGTCG ACAGGGACGG GGACTTTGCG 2940
gagctttacg tttcaAGTG GACTTCCCTT CTCACTCCCTC CGACCACCAT TCTGGTTGTG 3000
aacatgggtt ggatAGTGGC CGGCCTCTCG TTCGCCATCA ACAGTGGATA CCAGTCGTGG 3060
ggaccgctct tcggAAGGGT GTTCTTGCCT ATATGGGTAA TTGTCCTT GtACCCATTc 3120
cttaagggtt tgTTGGACG GcagaatCGG ACACCCACGA TTGTTATTG CTGGTCTGTA 3180
ctttggctt ccatatttcc tCTTCTATGG GTGCGTATTG ATCCGTTAC ATCGGACTCG 3240

```

acaaggctc gggggcaatg tggtatcgat tgctgagaat tgagattgtc ccgagtctgt 3300
tgttacagta aatagatggg catggccgcc atagagaaga tgaagaaggt aactactaa 3360
atggcgatcc acatgggtt aggctctgc cttcacaga caatgaggc caaagtgtt 3420
gatatgtcta ggttataatg tgttatacca actctaattt aaaacagtgt aatggattcc 3480
agaatgacga atgacttgtt cggttcaat tatttgaatt cctaaaaaac taatatctt 3540
tccccaaaaaaa aaaaaaaaaaaa aaa 3563

<210> 26
<211> 1091
<212> PRT
<213> Impatiens balsamia

<400> 26
Ala Arg Glu Ala Asn Ala Gly Leu Val Ala Gly Ser Tyr Lys Arg Asn
1 5 10 15

Glu Leu Val Arg Ile Arg His Asp Ser Asp Gly Gly Gln Pro Lys Pro
20 25 30

Leu Lys Glu Ala Asn Gly Gln Ile Cys Gln Ile Cys Gly Asp Thr Val
35 40 45

Gly Lys Ser Ala Thr Gly Asp Thr Phe Val Ala Cys Asn Glu Cys Gly
50 55 60

Phe Pro Val Cys Arg Pro Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Asn
65 70 75 80

Gln Cys Cys Pro Gln Cys Lys Thr Arg Tyr Lys Arg Gln Lys Gly Ser
85 90 95

Pro Arg Val Glu Gly Asp Glu Glu Glu Asp Val Asp Asp Leu Glu
100 105 110

Asn Glu Phe Asn Tyr Ser Gly Lys Gly Lys Asn Gln Lys Lys Val Thr
115 120 125

Thr Ala Arg Arg Pro Trp Gln Gly Asp Gln Gln Asp Ile Glu Leu Ser
130 135 140

Val Ser Ser Ser Arg His Asp Glu Ser Gln Gln Pro Val Pro Leu Leu
145 150 155 160

Thr His Gly His Ser Val Ser Gly Glu Ile Pro Thr Pro Asp Asn His
165 170 175

Ser Ile Arg Thr Thr Ser Gly Pro Ile Gly Pro Val Glu Lys Ser Ile
180 185 190

Pro Tyr Ile Asp Pro Arg Gln Pro Val Ala Val Arg Ile Ile Val Asp
195 200 205

Pro Ser Lys Asp Leu Asn Ser Tyr Gly Leu Gly Asn Val Asp Trp Lys
210 215 220

Glu Arg Val Glu Gly Trp Lys Leu Lys Gln Glu Lys Asn Met Val Gln
225 230 235 240

Met Thr Ser Arg Tyr Pro Glu Gly Lys Gly Asp Thr Glu Gly Thr Gly
 245 250 255
 Ser Asn Gly Glu Glu Leu Gln Met Ala Ala Asp Asp Ile Arg Gln Pro
 260 265 270
 Met Ser Arg Ile Val Pro Ile Ser Ser Thr His Leu Thr Pro Tyr Arg
 275 280 285
 Val Val Ile Ile Leu Arg Leu Ile Leu Gly Phe Phe Leu Gln Tyr
 290 295 300
 Arg Cys Thr His Pro Val Lys Asp Ala Tyr Pro Leu Trp Leu Thr Ser
 305 310 315 320
 Val Ile Cys Glu Val Trp Phe Ala Leu Ser Trp Leu Leu Asp Gln Phe
 325 330 335
 Pro Lys Trp Ser Pro Val Asn Arg Glu Thr Tyr Leu Asp Arg Leu Ser
 340 345 350
 Met Arg Phe Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala Pro Ile Asp
 355 360 365
 Val Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr
 370 375 380
 Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro Val Asp Lys
 385 390 395 400
 Val Ser Cys Tyr Val Ser Asp Asp Gly Ser Ala Met Leu Thr Phe Glu
 405 410 415
 Ala Leu Ser Glu Thr Ala Glu Phe Ala Lys Lys Trp Ala Pro Phe Cys
 420 425 430
 Lys Lys His Ser Ile Glu Pro Arg Ala Pro Glu Phe Tyr Phe Ala Gln
 435 440 445
 Lys Ile Asp Tyr Leu Lys Asp Lys Val Gln Pro Ser Phe Val Lys Glu
 450 455 460
 Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Val Arg Ile Asn
 465 470 475 480
 Ala Leu Val Ala Lys Ala Gln Lys Val Pro Glu Glu Gly Trp Thr Met
 485 490 495
 Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Ser Arg Asp His Pro Gly
 500 505 510
 Met Ile Gln Val Phe Leu Gly His Ser Gly Gly Phe Asp Thr Glu Gly
 515 520 525
 Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly
 530 535 540
 Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu Ile Arg Val
 545 550 555 560

ପ୍ରକାଶକ ପତ୍ର

Ser Ala Val Leu Thr Asn Gly Ala Tyr Leu Leu Asn Val Asp Cys Asp
 565 570 575
 His Tyr Phe Asn Asn Ser Lys Cys Leu Lys Glu Ala Met Cys Phe Met
 580 585 590
 Met Asp Pro Asn Leu Gly Lys Lys Thr Cys Tyr Val Gln Phe Pro Gln
 595 600 605
 Arg Phe Asp Gly Ile Asp Leu His Asp Arg Tyr Ala Asn Arg Asn Ile
 610 615 620
 Val Phe Phe Asp Ile Asn Leu Lys Gly Leu Asp Gly Ile Gln Gly Pro
 625 630 635 640
 Val Tyr Val Gly Thr Gly Cys Cys Phe Asn Arg Gln Ala Leu Tyr Gly
 645 650 655
 Tyr Asp Pro Val Leu Thr Glu Glu Asp Leu Glu Pro Asn Ile Ile Ile
 660 665 670
 Lys Ser Cys Cys Gly Ser Arg Lys Lys Gly Lys Gly Asn Lys Lys
 675 680 685
 Tyr Ile Asp Lys Asn Arg Ala Leu Lys Arg Thr Glu Ser Thr Ala Pro
 690 695 700
 Ile Phe Asn Met Glu Asp Ile Glu Glu Gly Ile Glu Gly Tyr Asp Asp
 705 710 715 720
 Glu Arg Ser Phe Leu Met Ala Gln Ser Tyr Glu Lys Arg Phe Gly Gln
 725 730 735
 Ser Pro Val Leu Ile Ala Ala Thr Phe Met Glu Gln Gly Gly Leu Pro
 740 745 750
 Pro Ser Thr Asn Ser Ala Thr Leu Leu Lys Glu Ala Ile His Val Ile
 755 760 765
 Ser Cys Gly Tyr Glu Asp Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp
 770 775 780
 Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly Phe Lys Met His
 785 790 795 800
 Thr Arg Gly Trp Ile Ser Ile Tyr Cys Met Pro Pro Arg Pro Ala Phe
 805 810 815
 Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu Asn Gln Val Leu
 820 825 830
 Arg Trp Ala Leu Gly Ser Ile Glu Ile Leu Leu Ser Arg His Cys Pro
 835 840 845
 Ile Trp Tyr Gly Tyr Ser Gly Arg Leu Lys Phe Leu Glu Arg Leu Ala
 850 855 860
 Tyr Ile Asn Thr Ile Val Tyr Pro Leu Thr Ser Ile Pro Leu Leu Ala
 865 870 875 880

Tyr Cys Thr Leu Pro Ala Ile Cys Leu Leu Thr Gly Lys Phe Ile Val
 885 890 895

 Pro Glu Ile Ser Asn Tyr Ala Ser Ile Trp Phe Ile Leu Leu Phe Val
 900 905 910

 Ser Ile Phe Ser Thr Gly Ile Leu Glu Leu Arg Trp Ser Gly Val Thr
 915 920 925

 Leu Glu Asp Trp Trp Arg Asn Glu Gln Phe Trp Val Ile Gly Gly Thr
 930 935 940

 Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu Lys Val Leu Ala
 945 950 955 960

 Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala Ser Asp Glu Asp
 965 970 975

 Gly Asp Phe Ala Glu Leu Tyr Val Phe Lys Trp Thr Ser Leu Leu Ile
 980 985 990

 Pro Pro Thr Thr Ile Leu Val Val Asn Met Val Gly Ile Val Ala Gly
 995 1000 1005

 Val Ser Phe Ala Ile Asn Ser Gly Tyr Gln Ser Trp Gly Pro Leu Phe
 1010 1015 1020

 Gly Arg Leu Phe Phe Ala Ile Trp Val Ile Val His Leu Tyr Pro Phe
 1025 1030 1035 1040

 Leu Lys Gly Leu Leu Gly Arg Gln Asn Arg Thr Pro Thr Ile Val Ile
 1045 1050 1055

 Val Trp Ser Val Leu Leu Ala Ser Ile Phe Ser Leu Leu Trp Val Arg
 1060 1065 1070

 Ile Asp Pro Phe Thr Ser Asp Ser Thr Lys Ala Arg Gly Gln Cys Gly
 1075 1080 1085

 Ile Asp Cys
 1090

<210> 27
 <211> 1560
 <212> DNA
 <213> Glycine max

<400> 27
 gcacgagggg aaggggaacc atcacagcta gcagctgttg acattttgt cagtaactgtt 60
 gatccattaa aagaacccc gcttgtact gctaacaactg tccttatctat tctttctgtt 120
 gactaccagg tgataaggct ctcctgttat gtctctgtat atgggtctgc tatgttgaca 180
 tttgaagctc tggtcgagac atcagaattt gctagggaaat gggttccttt cagcaagaaa 240
 tataatatcg aacctcgggc acctgagtgg tattttgcac agaagattga ctacttggaaa 300
 gataagggtt aaccatcatt tgtcaaagat cgttagagcaa tgaagagaga atatgaagaa 360
 tttaaaattc gcatcaatgg acttgttgca aaggcacaaa agattcctga agaaggatgg 420
 gtgtatgcaag atggtagcc atggccttgg aacaacacta gagaccatcc aggaatgatt 480
 caggtttct tggccaaag tggaggactt gacactgagg gtaatgaact tccacgttta 540
 gtctatgttt ctcgtaaaaa gcgtccaggg ttccaacatc acaagaaggc tggtgccatg 600
 aatgcacttg ttcgagtgtc agcagtcatt actaatggac ctttcttatt gaatcttgat 660

tgtgatcaact acataaaacaa cagtaaagcc ttgagggaag ctatgtgctt tatgtatggat 720
 cccaaccttg ggaaaaaatgt ttgctatgtc cagtttccac agaggtttga tggatttat 780
 aggaatgatc gatatgc当地 tcgcaataact gtttcttg atataaaactt gagaggttt 840
 gatggcattc aaggctc当地 ttatgtgggt actggatgtg tctttaatag aacagctt 900
 tatggctacg aaccccttat taaacccaag cataaaaagc ctgggtttct ttcttc当地 960
 tgtggggta accgaaagaa gagatcaaaa tctagcaaga aaggctcaga caagaaaaaa 1020
 tctagcaaga atgttgc当地 aactgtgccc atcttttagtc ttgaggatata agaagagggg 1080
 gtggaaaggta ctggatttga tcatgagaaa tcaactacta tgtcacaaat gggctcgag 1140
 aaaaggtttgc tgc当地 tgc当地 gc当地 tcatggagaa tggggc当地 1200
 cctc当地 tgc当地 caactccaga aactttctt aaggaaagcta ttcatgttat cagttgtt 1260
 tacgagata aatcagaatg gggaaagttagt gtagttagtta ccttatgttt aatggcttt 1320
 tatgttctt attccc当地 gcatctgtt atcagattaa tgtagcaga ttagtgc当地 1380
 ttcaggacc aaagatccaa tgaattaaac ttaaatatga taaagtatga acagtatagt 1440
 actgtctttt ttgagcctaa tatattaccc tctttgtaca gagttaaaag gggagctt 1500
 aatcttcc tttcttaagt aatgtgttagt atttc当地 aaaaaaaaaa aaaaaaaaaa 1560

<210> 28
 <211> 431
 <212> PRT
 <213> Glycine max

<400> 28
 Ala Arg Gly Glu Gly Glu Pro Ser Gln Leu Ala Ala Val Asp Ile Phe
 1 5 10 15

 Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro Leu Val Thr Ala Asn
 20 25 30

 Thr Val Leu Ser Ile Leu Ser Val Asp Tyr Pro Val Asp Lys Val Ser
 35 40 45

 Cys Tyr Val Ser Asp Asp Gly Ala Ala Met Leu Thr Phe Glu Ala Leu
 50 55 60

 Ala Glu Thr Ser Glu Phe Ala Arg Lys Trp Val Pro Phe Ser Lys Lys
 65 70 75 80

 Tyr Asn Ile Glu Pro Arg Ala Pro Glu Trp Tyr Phe Ala Gln Lys Ile
 85 90 95

 Asp Tyr Leu Lys Asp Lys Val Gln Pro Ser Phe Val Lys Asp Arg Arg
 100 105 110

 Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile Arg Ile Asn Gly Leu
 115 120 125

 Val Ala Lys Ala Gln Lys Ile Pro Glu Glu Gly Trp Val Met Gln Asp
 130 135 140

 Gly Thr Pro Trp Pro Gly Asn Asn Thr Arg Asp His Pro Gly Met Ile
 145 150 155 160

 Gln Val Phe Leu Gly Gln Ser Gly Gly Leu Asp Thr Glu Gly Asn Glu
 165 170 175

 Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys Arg Pro Gly Phe Gln
 180 185 190

His His Lys Lys Ala Gly Ala Met Asn Ala Leu Val Arg Val Ser Ala
 195 200 205
 Val Leu Thr Asn Gly Pro Phe Leu Leu Asn Leu Asp Cys Asp His Tyr
 210 215 220
 Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met Cys Phe Met Met Asp
 225 230 235 240
 Pro Asn Leu Gly Lys Asn Val Cys Tyr Val Gln Phe Pro Gln Arg Phe
 245 250 255
 Asp Gly Ile Asp Arg Asn Asp Arg Tyr Ala Asn Arg Asn Thr Val Phe
 260 265 270
 Phe Asp Ile Asn Leu Arg Gly Leu Asp Gly Ile Gln Gly Pro Val Tyr
 275 280 285
 Val Gly Thr Gly Cys Val Phe Asn Arg Thr Ala Leu Tyr Gly Tyr Glu
 290 295 300
 Pro Pro Ile Lys Pro Lys His Lys Lys Pro Gly Phe Leu Ser Ser Leu
 305 310 315 320
 Cys Gly Gly Asn Arg Lys Lys Arg Ser Lys Ser Ser Lys Lys Gly Ser
 325 330 335
 Asp Lys Lys Lys Ser Ser Lys Asn Val Asp Pro Thr Val Pro Ile Phe
 340 345 350
 Ser Leu Glu Asp Ile Glu Glu Gly Val Glu Gly Ala Gly Phe Asp Asp
 355 360 365
 Glu Lys Ser Leu Leu Met Ser Gln Met Ser Leu Glu Lys Arg Phe Gly
 370 375 380
 Gln Ser Ala Val Phe Val Ala Ser Thr Leu Met Glu Asn Gly Gly Val
 385 390 395 400
 Pro Gln Ser Ala Thr Pro Glu Thr Leu Leu Lys Glu Ala Ile His Val
 405 410 415
 Ile Ser Cys Gly Tyr Glu Asp Lys Ser Glu Trp Gly Ser Glu Val
 420 425 430

<210> 29
 <211> 3626
 <212> DNA
 <213> Triticum aestivum

<400> 29
 gcacgaggaa ccccgctcca gctctgtcgt cggtgcgggt tggatcgctc tgccgcgcc 60
 tggacggcga cgccggacgccc ctgaagtccg ggaggcacgg ggccggggac gtgtgccaga 120
 tctgcggcga cggcctgggc accacgttgg acggcgacgt cttcaccgccc tgcgacgtct 180
 gcccgttccc ggtctgccgc ccctgctacg agcacgagcgc caaggagggc acccaggcct 240
 gcctccagtgc caagaccaag tacaagcgcc acagagggag cccagcgtc cgcggggagg 300
 aaggcgcacga cactgatgccc gatgatggta gtgacttcaa ctaccctgca tctggcactg 360
 aggaccagaa gcagaagatt gctgacagagga tgcgccagctg ggcgcataac accggggggca 420
 gtggcaatgt tggccaccccc aagtatgaca gtggcgagat cggcctctcc aagtatgaca 480

gtggagat ccctaggaaa tacgtccctt cagtcaccaa cagccagatg tcaggagaaa
tcccgtggac ttcgcctgat catcacatga tgtcccctac gggaaacatc agcagacgtg 540
ctccgtttcc ctatgtaat cattcaccaa atccgtcaag ggagttctcc ggcagtattg 600
ggaatgtgc ctggaaagag agagtgatg gctggaaaat gaagcaggac aagggtgcga 660
ttccccatgac taatgggaca agcatgtctc cctctgaagg tcgggcagct actgacatcg 720
atgcatctac tgaatacacaac atggaagacg cttaactgaa tgatgaaact cgccagcctc 780
tatctagaaa agtccccatt gttccctcca aaataaaatcc ctacagaatg gtcatgttc 840
tgcggtttgt ttgttctaagc atcttctgc actaccgtct cacaatctt gtgcgtaatg 900
cataccact gtggctttta tctgttatg gtgagattt gttgtctta tcctggatac 960
tggatcagtt cccgaagtgg tttccaatca accgggagac ctaccttgat 1020
taaggtatga ccgagaaggt gaaccgtctc agttggctgc tgttgacata agactggctt 1080
cagtcgaccc ctgtgaaggag ccacccatcg tcaactgccaa cactgtgcta tttgtcagta 1140
ctgttgatc tcccggtggac aagggtcttt gctatgtatc tgatgacgga tccattttg 1200
tgactttga cgcattggct gagacttcag agtttgcgt gaaatgggtt gctcaatgc 1260
agaagtatga cattgaaccc agagctccc agttttactt tgccagaaa ccattttgt 1320
tgaaagacaa agtccagccct tcattttgtt aagaccgcg ggcattgtt attgattacc 1380
aagaatttaa aatcaggata aatgccctag tttcttaaggc attgaaagtc agagaatatg 1440
gatggatcat gcaagatggc acaccatggc cagggaaacaa taccagggtt cccgaggaa 1500
tgattcaggt ttcccttgggt cacagtggc gccttgatc tgagggtat gatcccccc 1560
gttttagttt tggtgtctcg taaaagcgtc ctgggttcca gcaccacaaag gagctcccc 1620
ccatgaatgc ccttgcgtgt gtctcagctg tccttactaa tggacaatac atgttgaatc 1680
ttgatttgta tcactacatc aacaacagca aggctgtccg agaagctatg tgcttcttaa 1740
tggatccaaa cctaggtccg caagtcgtt atgtgcagtt cccacaaagg tttgtatggg 1800
ttgatagggaa ttagtgcataat gcaaacaggaa acactgtctt ttttgatatt aacttgagg 1860
gccttgcacgg cattcaaggg ctagttatg tgggaaactgg ttgtgtttt aacagaacag 1920
ctatctatgg ttatgagccca ccaattaagg ogaagaagcc aggtttcttg gcatcactat 1980
gtggggccaa gaagaaggca agcaagtcaa agaaaaggag ctcagataag aaaaagtgc 2040
acaagcatgt ggacagttct gttccagttat tcaatctcg agacatagag gagggtgtt 2100
aagggtctgg gtttgatgtat gagaatctcg ttctcatgtc tcaaatacgcc ttagagaaga 2160
gatttggcca gtcagcagca ttgttgccct ccactctgtat ggaatatggg ggtgttcctc 2220
agtcctccac tccagaatct ctttgaaaag aagctatcca tgcataatgt tgcgtatgt 2280
aggacaagtc tgaatggggaa actgagattt gttggatcta tggatctgtc acagaagata 2340
ttcttactgg attcaagatg cacgcaagag gctggcgctc agtctattgc atgcccac 2400
gcccagctt caagggatct gccccatca atcttcaaga tcgtctgaac caagtgcgtc 2460
ggtgggtctc cgttctgtt gaaattctt tcagccggca ttgcccctt tggtatggc 2520
acggaggcg cctcaagttc ctggagagat tcgcttacat caacaccacc attaccac 2580
taacctctc cccgcttcta gtctattgtt tattgcctgc tatctgtctg ctcactggaa 2640
agttcatcat gccagagatt agcaacttgg ccagttatctg gttcattgcg ctcttcctt 2700
caatttcgc cactggatc cttgagatga gttggagttt tggtggcatt gacgagtgtt 2760
ggaggaatga acagttctgg gtcattggag gtatctctgc acatctgtt tcaaggcttc 2820
agggtcttct gaaggtgttt gcccgtatcg acaccaactt cactgtcacc tcaaaggcta 2880
atgacgaaga aggcgacttt gctgagctct acatgttcaa gtggacgacg cttctcatcc 2940
ctccgacgac cattttgatc attaacatgg ttgggtgtctg tgctggcacc tcctacgcca 3000
tcaacagtgg ttaccaatca tggggccgc tctttggaa gctttcttt gccttctggg 3060
tgattgttca ctatataccca ttccctcaagg gtcttatggg caggcaaaac cgcacaccga 3120
cgattgtcat cgtctgggtt gtcctctcg ttcttatctt ctccttgctg tgggtcgtg 3180
ttgatcattt cactaccgt ctgcgtggcc caaatatcca aacottgtggc atcaactgt 3240
aggaaagtgg gagttttagt ggggtgtgaa ttactacgtt tgagaaagtt aaccggcgg 3300
gccagagaat atttatgttg agaaaacaca ttgttaata gatgtatag accatctacc gtttcatga 3360
ttctttttt ggaacaaagg aatctcattt gtaaaacctat aggaattttc gtttaagctc 3420
cttggattt taggaatggc cctatgaaaat gttgtattt ttattttat aaattattcc 3480
tgtccttcac attttggagg agtttt

<210> 30
<211> 1080
<212> PRT
<213> *Triticum aestivum*

<400> 30
 Met Asp Gly Asp Ala Asp Ala Leu Lys Ser Gly Arg His Gly Ala Gly
 1 5 10 15

 Asp Val Cys Gln Ile Cys Ala Asp Gly Leu Gly Thr Thr Leu Asp Gly
 20 25 30

 Asp Val Phe Thr Ala Cys Asp Val Cys Arg Phe Pro Val Cys Arg Pro
 35 40 45

 Cys Tyr Glu His Glu Arg Lys Glu Gly Thr Gln Ala Cys Leu Gln Cys
 50 55 60

 Lys Thr Lys Tyr Lys Arg His Arg Gly Ser Pro Ala Ile Arg Gly Glu
 65 70 75 80

 Glu Gly Asp Asp Thr Asp Ala Asp Asp Gly Ser Asp Phe Asn Tyr Pro
 85 90 95

 Ala Ser Gly Thr Glu Asp Gln Lys Gln Lys Ile Ala Asp Arg Met Arg
 100 105 110

 Ser Trp Arg Met Asn Thr Gly Gly Ser Gly Asn Val Gly His Pro Lys
 115 120 125

 Tyr Asp Ser Gly Glu Ile Gly Leu Ser Lys Tyr Asp Ser Gly Glu Ile
 130 135 140

 Pro Arg Gly Tyr Val Pro Ser Val Thr Asn Ser Gln Met Ser Gly Glu
 145 150 155 160

 Ile Pro Gly Ala Ser Pro Asp His His Met Met Ser Pro Thr Gly Asn
 165 170 175

 Ile Ser Arg Arg Ala Pro Phe Pro Tyr Val Asn His Ser Pro Asn Pro
 180 185 190

 Ser Arg Glu Phe Ser Gly Ser Ile Gly Asn Val Ala Trp Lys Glu Arg
 195 200 205

 Val Asp Gly Trp Lys Met Lys Gln Asp Lys Gly Ala Ile Pro Met Thr
 210 215 220

 Asn Gly Thr Ser Ile Ala Pro Ser Glu Gly Arg Ala Ala Thr Asp Ile
 225 230 235 240

 Asp Ala Ser Thr Glu Tyr Asn Met Glu Asp Ala Leu Leu Asn Asp Glu
 245 250 255

 Thr Arg Gln Pro Leu Ser Arg Lys Val Pro Ile Ala Ser Ser Lys Ile
 260 265 270

 Asn Pro Tyr Arg Met Val Ile Val Leu Arg Leu Val Val Leu Ser Ile
 275 280 285

 Phe Leu His Tyr Arg Leu Thr Asn Pro Val Arg Asn Ala Tyr Pro Leu
 290 295 300

 Trp Leu Leu Ser Val Ile Cys Glu Ile Trp Phe Ala Leu Ser Trp Ile
 305 310 315 320

DRAFT 2005-09

Leu	Asp	Gln	Phe	Pro	Lys	Trp	Phe	Pro	Ile	Asn	Arg	Glu	Thr	Tyr	Leu
325															335
Asp	Arg	Leu	Ala	Leu	Arg	Tyr	Asp	Arg	Glu	Gly	Glu	Pro	Ser	Gln	Leu
340															350
Ala	Ala	Val	Asp	Ile	Phe	Val	Ser	Thr	Val	Asp	Pro	Leu	Lys	Glu	Pro
355															365
Pro	Ile	Val	Thr	Ala	Asn	Thr	Val	Leu	Ser	Ile	Leu	Ala	Val	Asp	Tyr
370															380
Pro	Val	Asp	Lys	Val	Ser	Cys	Tyr	Val	Ser	Asp	Asp	Gly	Ala	Ser	Met
385															400
Leu	Thr	Phe	Asp	Ala	Leu	Ala	Glu	Thr	Ser	Glu	Phe	Ala	Arg	Lys	Trp
405															415
Val	Pro	Phe	Val	Lys	Lys	Tyr	Asp	Ile	Glu	Pro	Arg	Ala	Pro	Glu	Phe
420															430
Tyr	Phe	Cys	Gln	Lys	Ile	Asp	Tyr	Leu	Lys	Asp	Lys	Val	Gln	Pro	Ser
435															445
Phe	Val	Lys	Asp	Arg	Arg	Ala	Met	Lys	Arg	Glu	Tyr	Glu	Glu	Phe	Lys
450															460
Ile	Arg	Ile	Asn	Ala	Leu	Val	Ser	Lys	Ala	Leu	Lys	Val	Pro	Glu	Glu
465															480
Gly	Trp	Ile	Met	Gln	Asp	Gly	Thr	Pro	Trp	Pro	Gly	Asn	Asn	Thr	Arg
485															495
Asp	His	Pro	Gly	Met	Ile	Gln	Val	Phe	Leu	Gly	His	Ser	Gly	Gly	Leu
500															510
Asp	Thr	Glu	Gly	Asn	Glu	Leu	Pro	Arg	Leu	Val	Tyr	Val	Ser	Arg	Glu
515															525
Lys	Arg	Pro	Gly	Phe	Gln	His	His	Lys	Lys	Ala	Gly	Ala	Met	Asn	Ala
530															540
Leu	Val	Arg	Val	Ser	Ala	Val	Leu	Thr	Asn	Gly	Gln	Tyr	Met	Leu	Asn
545															560
Leu	Asp	Cys	Asp	His	Tyr	Ile	Asn	Asn	Ser	Lys	Ala	Val	Arg	Glu	Ala
565															575
Met	Cys	Phe	Leu	Met	Asp	Pro	Asn	Leu	Gly	Pro	Gln	Val	Cys	Tyr	Val
580															590
Gln	Phe	Pro	Gln	Arg	Phe	Asp	Gly	Ile	Asp	Arg	Asn	Asp	Arg	Tyr	Ala
595															605
Asn	Arg	Asn	Thr	Val	Phe	Phe	Asp	Ile	Asn	Leu	Arg	Gly	Leu	Asp	Gly
610															620
Ile	Gln	Gly	Pro	Val	Tyr	Val	Gly	Thr	Gly	Cys	Val	Phe	Asn	Arg	Thr
625															640

DRAFT

Ala Ile Tyr Gly Tyr Glu Pro Pro Ile Lys Ala Lys Lys Pro Gly Phe
645 650 655

Leu Ala Ser Leu Cys Gly Gly Lys Lys Lys Ala Ser Lys Ser Lys Lys
660 665 670

Arg Ser Ser Asp Lys Lys Ser Asn Lys His Val Asp Ser Ser Val
675 680 685

Pro Val Phe Asn Leu Glu Asp Ile Glu Glu Gly Val Glu Gly Ala Gly
690 695 700

Phe Asp Asp Glu Lys Ser Val Leu Met Ser Gln Met Ser Leu Glu Lys
705 710 715 720

Arg Phe Gly Gln Ser Ala Ala Phe Val Ala Ser Thr Leu Met Glu Tyr
725 730 735

Gly Gly Val Pro Gln Ser Ser Thr Pro Glu Ser Leu Leu Lys Glu Ala
740 745 750

Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys Ser Glu Trp Gly Thr
755 760 765

Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr Gly
770 775 780

Phe Lys Met His Ala Arg Gly Trp Arg Ser Val Tyr Cys Met Pro Lys
785 790 795 800

Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg Leu
805 810 815

Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu Phe Ser
820 825 830

Arg His Cys Pro Leu Trp Tyr Gly Tyr Gly Arg Leu Lys Phe Leu
835 840 845

Glu Arg Phe Ala Tyr Ile Asn Thr Thr Ile Tyr Pro Leu Thr Ser Leu
850 855 860

Pro Leu Leu Val Tyr Cys Ile Leu Pro Ala Ile Cys Leu Leu Thr Gly
865 870 875 880

Lys Phe Ile Met Pro Glu Ile Ser Asn Leu Ala Ser Ile Trp Phe Ile
885 890 895

Ala Leu Phe Leu Ser Ile Phe Ala Thr Gly Ile Leu Glu Met Arg Trp
900 905 910

Ser Gly Val Gly Ile Asp Glu Trp Trp Arg Asn Glu Gln Phe Trp Val
915 920 925

Ile Gly Gly Ile Ser Ala His Leu Phe Ala Val Phe Gln Gly Leu Leu
930 935 940

Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys Ala
945 950 955 960

Asn Asp Glu Glu Gly Asp Phe Ala Glu Leu Tyr Met Phe Lys Trp Thr
 965 970 975
 Thr Leu Leu Ile Pro Pro Thr Thr Ile Leu Ile Ile Asn Met Val Gly
 980 985 990
 Val Val Ala Gly Thr Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser Trp
 995 1000 1005
 Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val His
 1010 1015 1020
 Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr Pro
 1025 1030 1035 1040
 Thr Ile Val Ile Val Trp Ala Val Leu Leu Ala Ser Ile Phe Ser Leu
 1045 1050 1055
 Leu Trp Val Arg Val Asp Pro Phe Thr Thr Arg Leu Ala Gly Pro Asn
 1060 1065 1070
 Ile Gln Thr Cys Gly Ile Asn Cys
 1075 1080

 <210> 31
 <211> 685
 <212> PRT
 <213> *Gossypium hirsutum*

 <400> 31
 Arg Arg Trp Val Pro Phe Cys Lys Lys His Asn Val Glu Pro Arg Ala
 1 5 10 15

 Pro Glu Phe Tyr Phe Asn Glu Lys Ile Asp Tyr Leu Lys Asp Lys Val
 20 25 30

 His Pro Ser Phe Val Lys Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu
 35 40 45

 Glu Phe Lys Val Arg Ile Asn Ala Leu Val Ala Lys Ala Gln Lys Lys
 50 55 60

 Pro Glu Glu Gly Trp Val Met Gln Asp Gly Thr Pro Trp Pro Gly Asn
 65 70 75 80

 Asn Thr Arg Asp His Pro Gly Met Ile Gln Val Tyr Leu Gly Ser Ala
 85 90 95

 Gly Ala Leu Asp Val Asp Gly Lys Glu Leu Pro Arg Leu Val Tyr Val
 100 105 110

 Ser Arg Glu Lys Arg Pro Gly Tyr Gln His His Lys Lys Ala Gly Ala
 115 120 125

 Glu Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Ala Pro Phe
 130 135 140

Ile Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Met
 145 150 155 160
 Arg Glu Ala Met Cys Phe Leu Met Asp Pro Gln Phe Gly Lys Lys Leu
 165 170 175
 Cys Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg His Asp
 180 185 190
 Arg Tyr Ala Asn Arg Asn Val Val Phe Phe Asp Ile Asn Met Leu Gly
 195 200 205
 Leu Asp Gly Leu Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe
 210 215 220
 Asn Arg Gln Ala Leu Tyr Gly Tyr Asp Pro Pro Val Ser Glu Lys Arg
 225 230 235 240
 Pro Lys Met Thr Cys Asp Cys Trp Pro Ser Trp Cys Cys Cys Cys Cys
 245 250 255
 Gly Gly Ser Arg Lys Lys Ser Lys Lys Lys Gly Glu Lys Lys Gly Leu
 260 265 270
 Leu Gly Gly Leu Leu Tyr Gly Lys Lys Lys Lys Met Met Gly Lys Asn
 275 280 285
 Tyr Val Lys Lys Gly Ser Ala Pro Val Phe Asp Leu Glu Glu Ile Glu
 290 295 300
 Glu Gly Leu Glu Gly Tyr Glu Glu Leu Glu Lys Ser Thr Leu Met Ser
 305 310 315 320
 Gln Lys Asn Phe Glu Lys Arg Phe Gly Gln Ser Pro Val Phe Ile Ala
 325 330 335
 Ser Thr Leu Met Glu Asn Gly Gly Leu Pro Glu Gly Thr Asn Ser Thr
 340 345 350
 Ser Leu Ile Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Glu
 355 360 365
 Lys Thr Glu Trp Gly Lys Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr
 370 375 380
 Glu Asp Ile Leu Thr Gly Phe Lys Met His Cys Arg Gly Trp Lys Ser
 385 390 395 400
 Val Tyr Cys Val Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile
 405 410 415
 Asn Leu Ser Asp Arg Leu His Gln Val Leu Arg Trp Ala Leu Gly Ser
 420 425 430
 Val Glu Ile Phe Leu Ser Arg His Cys Pro Leu Trp Tyr Gly Tyr Gly
 435 440 445
 Gly Lys Leu Lys Trp Leu Glu Arg Leu Ala Tyr Ile Asn Thr Ile Val
 450 455 460

Tyr Pro Phe Thr Ser Ile Pro Leu Leu Ala Tyr Cys Thr Ile Pro Ala
 465 470 475 480
 Val Cys Leu Leu Thr Gly Lys Phe Ile Ile Pro Thr Leu Ser Asn Leu
 485 490 495
 Thr Ser Val Trp Phe Leu Ala Leu Phe Leu Ser Ile Ile Ala Thr Gly
 500 505 510
 Val Leu Glu Leu Arg Trp Ser Gly Val Ser Ile Gln Asp Trp Trp Arg
 515 520 525
 Asn Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe Ala
 530 535 540
 Val Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Val Asp Thr Asn Phe
 545 550 555 560
 Thr Val Thr Ala Lys Ala Ala Asp Asp Thr Glu Phe Gly Glu Leu Tyr
 565 570 575
 Leu Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Ile Ile
 580 585 590
 Leu Asn Met Val Gly Val Val Ala Gly Val Ser Asp Ala Ile Asn Asn
 595 600 605
 Gly Tyr Gly Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe
 610 615 620
 Trp Val Ile Leu His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg
 625 630 635 640
 Gln Asn Arg Thr Pro Thr Ile Val Val Leu Trp Ser Ile Leu Ala
 645 650 655
 Ser Ile Phe Ser Leu Val Trp Val Arg Ile Asp Pro Phe Leu Pro Lys
 660 665 670
 Gln Thr Gly Pro Val Leu Lys Gln Cys Gly Val Glu Cys
 675 680 685

 <210> 32
 <211> 701
 <212> PRT
 <213> *Gossypium hirsutum*

 <400> 32
 Asp Tyr Pro Val Glu Lys Val Ser Cys Tyr Val Ser Asp Asp Gly Ala
 1 5 10 15

 Ala Met Leu Thr Phe Glu Ala Leu Ser Glu Thr Ser Glu Phe Ala Arg
 20 25 30

 Lys Trp Val Pro Phe Cys Lys Lys Tyr Asn Ile Glu Pro Arg Ala Pro
 35 40 45

 Glu Trp Tyr Phe Ala Gln Lys Ile Asp Tyr Leu Lys Asp Lys Val Gln
 50 55 60

Thr Ser Phe Val Lys Glu Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu
 65 70 75 80
 Phe Lys Val Arg Val Asn Gly Leu Val Ala Lys Ala Gln Lys Val Pro
 85 90 95
 Glu Glu Gly Trp Ile Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn
 100 105 110
 Thr Arg Asp His Pro Gly Met Ile Gln Val Phe Leu Gly Gln Ser Gly
 115 120 125
 Gly Leu Asp Ala Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser
 130 135 140
 Arg Glu Lys Arg Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met
 145 150 155 160
 Asn Ala Leu Val Arg Val Ser Ala Val Leu Thr Asn Gly Ala Phe Leu
 165 170 175
 Leu Asn Leu Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Leu Arg
 180 185 190
 Glu Ala Met Cys Phe Leu Met Asp Pro Asn Leu Gly Lys Gln Val Cys
 195 200 205
 Tyr Val Gln Phe Pro Gln Arg Phe Asp Gly Ile Asp Arg Asn Asp Arg
 210 215 220
 Tyr Ala Asn Arg Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu
 225 230 235 240
 Asp Gly Ile Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn
 245 250 255
 Arg Thr Ala Leu Tyr Gly Tyr Glu Pro Pro Leu Lys Pro Lys His Arg
 260 265 270
 Lys Thr Gly Ile Leu Ser Ser Leu Cys Gly Gly Ser Arg Lys Lys Ser
 275 280 285
 Ser Lys Ser Ser Lys Lys Gly Ser Asp Lys Lys Ser Gly Lys His
 290 295 300
 Val Asp Ser Thr Val Pro Val Phe Asn Leu Glu Asp Ile Glu Glu Gly
 305 310 315 320
 Val Glu Gly Ala Gly Phe Asp Asp Glu Lys Ser Leu Leu Met Ser Gln
 325 330 335
 Met Ser Leu Glu Lys Arg Phe Gly Gln Ser Ala Val Phe Val Ala Ser
 340 345 350
 Thr Leu Met Glu Asn Gly Gly Val Pro Gln Ser Ala Thr Pro Glu Thr
 355 360 365
 Leu Leu Lys Glu Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys
 370 375 380

E06020-0200660

Thr Asp Trp Gly Ser Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu
385 390 395 400

Asp Ile Leu Thr Gly Phe Lys Met His Ala Arg Gly Trp Arg Ser Ile
405 410 415

Tyr Cys Met Pro Lys Arg Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn
420 425 430

Leu Ser Asp Arg Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Val
435 440 445

Glu Ile Leu Phe Ser Arg His Cys Pro Ile Trp Tyr Gly Tyr Ser Gly
450 455 460

Arg Leu Lys Trp Leu Glu Arg Phe Ala Tyr Val Asn Thr Thr Ile Tyr
465 470 475 480

Pro Val Thr Ala Ile Pro Leu Leu Met Tyr Cys Thr Leu Pro Ala Val
485 490 495

Cys Leu Leu Thr Asn Lys Phe Ile Ile Pro Gln Ile Ser Asn Leu Ala
500 505 510

Ser Ile Trp Phe Ile Ser Leu Phe Leu Ser Ile Phe Ala Thr Gly Ile
515 520 525

Leu Lys Met Lys Trp Asn Gly Val Gly Ile Asp Gln Trp Trp Arg Asn
530 535 540

Glu Gln Phe Trp Val Ile Gly Gly Val Ser Ala His Leu Phe Ala Val
545 550 555 560

Phe Gln Gly Leu Leu Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr
565 570 575

Val Thr Ser Lys Ala Ser Asp Glu Asp Gly Asp Phe Ala Glu Leu Tyr
580 585 590

Met Phe Lys Trp Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Ile
595 600 605

Ile Asn Leu Val Gly Val Val Ala Gly Ile Ser Tyr Val Ile Asn Ser
610 615 620

Gly Tyr Gln Ser Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe
625 630 635 640

Trp Val Ile Ile His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg
645 650 655

Gln Asn Arg Thr Pro Thr Ile Val Val Val Trp Ser Ile Leu Leu Ala
660 665 670

Ser Ile Phe Ser Leu Leu Trp Val Arg Ile Asp Pro Phe Thr Thr Arg
675 680 685

Val Thr Gly Pro Asp Val Glu Gln Cys Gly Ile Asn Cys
690 695 700

<210> 33
 <211> 1065
 <212> PRT
 <213> Arabidopsis thaliana

<400> 33
 Met Glu Ser Glu Gly Glu Thr Ala Gly Lys Pro Met Lys Asn Ile Val
 1 5 10 15

Pro Gln Thr Cys Gln Ile Cys Ser Asp Asn Val Gly Lys Thr Val Asp
 20 25 30

Gly Asp Arg Phe Val Ala Cys Asp Ile Cys Ser Phe Pro Val Cys Arg
 35 40 45

Pro Cys Tyr Glu Tyr Glu Arg Lys Asp Gly Asn Gln Ser Cys Pro Gln
 50 55 60

Cys Lys Thr Arg Tyr Lys Arg Leu Lys Gly Ser Pro Ala Ile Pro Gly
 65 70 75 80

Asp Lys Asp Glu Asp Gly Leu Ala Asp Glu Gly Thr Val Glu Phe Asn
 85 90 95

Tyr Pro Gln Lys Glu Lys Ile Ser Glu Arg Met Leu Gly Trp His Leu
 100 105 110

Thr Arg Gly Lys Gly Glu Glu Met Gly Glu Pro Gln Tyr Asp Lys Glu
 115 120 125

Val Ser His Asn His Leu Pro Arg Leu Thr Ser Arg Gln Asp Thr Ser
 130 135 140

Gly Glu Phe Ser Ala Ala Ser Pro Glu Arg Leu Ser Val Ser Ser Thr
 145 150 155 160

Ile Ala Gly Gly Lys Arg Leu Pro Tyr Ser Ser Asp Val Asn Gln Ser
 165 170 175

Pro Asn Arg Arg Ile Val Asp Pro Val Gly Leu Gly Asn Val Ala Trp
 180 185 190

Lys Glu Arg Val Asp Gly Trp Lys Met Lys Gln Glu Lys Asn Thr Gly
 195 200 205

Pro Val Ser Thr Gln Ala Ala Ser Glu Arg Gly Gly Val Asp Ile Asp
 210 215 220

Ala Ser Thr Asp Ile Leu Ala Asp Glu Ala Leu Leu Asn Asp Glu Ala
 225 230 235 240

Arg Gln Pro Leu Ser Arg Lys Val Ser Ile Pro Ser Ser Arg Ile Asn
 245 250 255

Pro Tyr Arg Met Val Ile Met Leu Arg Leu Val Ile Leu Cys Leu Phe
 260 265 270

Leu His Tyr Arg Ile Thr Asn Pro Val Pro Asn Ala Phe Ala Leu Trp
 275 280 285
 Leu Val Ser Val Ile Cys Glu Ile Trp Phe Ala Leu Ser Trp Ile Leu
 290 295 300
 Asp Gln Phe Pro Lys Trp Phe Pro Val Asn Arg Glu Thr Tyr Leu Asp
 305 310 315 320
 Arg Leu Ala Leu Arg Tyr Asp Arg Glu Gly Glu Pro Ser Gln Leu Ala
 325 330 335
 Ala Val Asp Ile Phe Val Ser Thr Val Asp Pro Leu Lys Glu Pro Pro
 340 345 350
 Leu Val Thr Ala Asn Thr Val Leu Ser Ile Leu Ala Val Asp Tyr Pro
 355 360 365
 Val Asp Lys Val Ser Cys Tyr Val Phe Asp Asp Gly Ala Ala Met Leu
 370 375 380
 Ser Phe Glu Ser Leu Ala Glu Thr Ser Glu Phe Ala Arg Lys Trp Val
 385 390 395 400
 Pro Phe Cys Lys Lys Tyr Ser Ile Glu Pro Arg Ala Pro Glu Trp Tyr
 405 410 415
 Phe Ala Ala Lys Ile Asp Tyr Leu Lys Asp Lys Val Gln Thr Ser Phe
 420 425 430
 Val Lys Asp Arg Arg Ala Met Lys Arg Glu Tyr Glu Glu Phe Lys Ile
 435 440 445
 Arg Ile Asn Ala Leu Val Ser Lys Ala Leu Lys Cys Pro Glu Glu Gly
 450 455 460
 Trp Val Met Gln Asp Gly Thr Pro Trp Pro Gly Asn Asn Thr Gly Asp
 465 470 475 480
 His Pro Gly Met Ile Gln Val Phe Leu Gly Gln Asn Gly Gly Leu Asp
 485 490 495
 Ala Glu Gly Asn Glu Leu Pro Arg Leu Val Tyr Val Ser Arg Glu Lys
 500 505 510
 Arg Pro Gly Phe Gln His His Lys Lys Ala Gly Ala Met Asn Ala Leu
 515 520 525
 Val Arg Val Ser Ala Val Leu Thr Asn Gly Pro Phe Ile Leu Asn Leu
 530 535 540
 Asp Cys Asp His Tyr Ile Asn Asn Ser Lys Ala Leu Arg Glu Ala Met
 545 550 555 560
 Cys Phe Leu Met Asp Pro Asn Leu Gly Lys Gln Val Cys Tyr Val Gln
 565 570 575
 Phe Pro Gln Arg Phe Asp Gly Ile Asp Lys Asn Asp Arg Tyr Ala Asn
 580 585 590

Arg Asn Thr Val Phe Phe Asp Ile Asn Leu Arg Gly Leu Asp Gly Ile
595 600 605

Gln Gly Pro Val Tyr Val Gly Thr Gly Cys Val Phe Asn Arg Thr Ala
610 615 620

Leu Tyr Gly Tyr Glu Pro Pro Ile Lys Val Lys His Lys Lys Pro Ser
625 630 635 640

Leu Leu Ser Lys Leu Cys Gly Ser Arg Lys Lys Asn Ser Lys Ala
645 650 655

Lys Lys Glu Ser Asp Lys Lys Ser Gly Arg His Thr Asp Ser Thr
660 665 670

Val Pro Val Phe Asn Leu Asp Asp Ile Glu Glu Gly Val Glu Gly Ala
675 680 685

Gly Phe Asp Asp Glu Lys Ala Leu Leu Met Ser Gln Met Ser Leu Glu
690 695 700

Lys Arg Phe Gly Gln Ser Ala Val Phe Val Ala Ser Thr Leu Met Glu
705 710 715 720

Asn Gly Gly Val Pro Pro Ser Ala Thr Pro Glu Asn Leu Leu Lys Glu
725 730 735

Ala Ile His Val Ile Ser Cys Gly Tyr Glu Asp Lys Ser Asp Trp Gly
740 745 750

Met Glu Ile Gly Trp Ile Tyr Gly Ser Val Thr Glu Asp Ile Leu Thr
755 760 765

Gly Phe Lys Met His Ala Arg Gly Trp Arg Ser Ile Tyr Cys Met Pro
770 775 780

Lys Leu Pro Ala Phe Lys Gly Ser Ala Pro Ile Asn Leu Ser Asp Arg
785 790 795 800

Leu Asn Gln Val Leu Arg Trp Ala Leu Gly Ser Val Glu Ile Leu Phe
805 810 815

Ser Arg His Cys Pro Ile Trp Tyr Gly Tyr Asn Gly Arg Leu Lys Phe
820 825 830

Leu Glu Arg Phe Ala Tyr Val Asn Thr Thr Ile Tyr Pro Ile Thr Ser
835 840 845

Ile Pro Leu Leu Met Tyr Cys Thr Leu Leu Ala Val Cys Leu Phe Thr
850 855 860

Asn Gln Phe Ile Ile Pro Gln Ile Ser Asn Ile Ala Ser Ile Trp Phe
865 870 875 880

Leu Ser Leu Phe Leu Ser Ile Phe Ala Thr Gly Ile Leu Glu Met Arg
885 890 895

Trp Ser Gly Val Gly Ile Asp Glu Trp Trp Arg Asn Glu Gln Phe Trp
900 905 910

Val Ile Gly Gly Val Ser Ala His Leu Phe Ala Val Phe Gln Gly Ile
915 920 925

Leu Lys Val Leu Ala Gly Ile Asp Thr Asn Phe Thr Val Thr Ser Lys
930 935 940

Ala Ser Asp Glu Asp Gly Asp Phe Ala Glu Leu Tyr Leu Phe Lys Trp
945 950 955 960

Thr Thr Leu Leu Ile Pro Pro Thr Thr Leu Leu Ile Val Asn Leu Val
965 970 975

Gly Val Val Ala Gly Val Ser Tyr Ala Ile Asn Ser Gly Tyr Gln Ser
980 985 990

Trp Gly Pro Leu Phe Gly Lys Leu Phe Phe Ala Phe Trp Val Ile Val
995 1000 1005

His Leu Tyr Pro Phe Leu Lys Gly Leu Met Gly Arg Gln Asn Arg Thr
1010 1015 1020

Pro Thr Ile Val Val Val Trp Ser Val Leu Leu Ala Ser Ile Phe Ser
1025 1030 1035 1040

Leu Leu Trp Val Arg Ile Asp Pro Phe Thr Ser Arg Val Thr Gly Pro
1045 1050 1055

Asp Ile Leu Glu Cys Gly Ile Asn Cys
1060 1065